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87.287 Million cell updates/sec
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ado34231 Synthetic	ľ	Ado34228 Synthetic	9	6	4	4	Ado34338 Synthetic	N	0	Ado34339 Synthetic	7	Ado34244 Synthetic	Ado34276 Synthetic	Ado34227 Synthetic	Ado34350 Synthetic	Ado34322 Synthetic	Ado34336 Synthetic	D.	7	Ado34241 Synthetic	Ado34240 Synthetic	Ado34284 Synthetic
SUMMARIES	ΙD	AD034231	AD034225	AD034228	AD034236	ADO34233	ADO34314	ADO34354	AD034338	AD034352	ADO34340	AD034339	AD034297	ADO34244	AD034276	AD034227	ADO34350	AD034322	AD034336	AD034335	AD034337	AD034241	ADO34240	AD034284
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RESULT 1

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summaries

Post-processing: Minimum Match 0% Maximum Match 100%

Maximum Match 100 Listing first 45

A Geneseq 8:\* 1: geneseqp19

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Database

ADO34231 standard; peptide; 18 AA.

ADO34231;

(first entry) 12-AUG-2004 Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 8.

apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina. low-density lipoprotein; LDL; very low density lipoprotein; UDL; 

Synthetic.

WO2004043403-A2.

27-MAY-2004.

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P.

(UABR-) UAB RES FOUND.

Datta G; Garber DW, Anantharamiah GM,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 8; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypucleotide, a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and acrier; and an monoclonal antibody that specifically binds to the synthetic

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apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antiandinal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein-E mimicking mimicking polypeptide of the invention.
            8x88888888888888888888888888888888
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Gaps ö 100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 6.4e-08; 0; Mismatches GIRRFLGSIWRFIRAFYG 18 1 GIRRFLGSIWRFIRAFYG 18 Local Similarity 100. Query Match Best Loca Matches ò

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AD034225

ADO34225 standard; peptide; 18 AA. AD034225;

(first entry) 12-AUG-2004 Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholestreol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL. 

Synthetic

'note= "N-terminal acetyl" /note= "C-terminal amide" Location/Qualifiers Modified-site

WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

Datta G; Garber DW, WPI; 2004-411629/38. Anantharamiah GM,

Claim 4; SEQ ID NO 2; 79pp; English

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject

Claim 4; SEQ ID NO 5; 79pp; English.

ö cuch as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for treating coronary artery disease, my dysbetaliapoprotehaemia or atheroscalerosis, and for reducing the risk of and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention. a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymuclectide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide activities: antilipaemic, cardiant, vasótrópic, antiarteriosclerótic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasctropic; antiarreriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina, low-density lipoprotein; LDL; very low density lipoprotein; VLDL. Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. Gaps ö Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 5. 100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 6.4e-08; 0; Indels Mismatches ö Datta ADO34228 standard; peptide; 18 AA. ö 1 GIRRFLGSIWRFIRAFYG 18 1 GIRRFLGSIWRFIRAFYG 18 Garber DW, 13-NOV-2003; 2003WO-US036268 13-NOV-2002; 2002US-0425821P Query Match
Best Local Similarity 100.0
Watches 18; Conservative 12-AUG-2004 (first entry) (UABR-) UAB RES FOUND WPI; 2004-411629/38. Anantharamiah GM, Sequence 18 AA; WO2004043403-A2 27-MAY-2004. ADO34228; RESULT 3 g 

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mimicking polypeptide encoding polymclectide; accomposition comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymclectide; and a carrier; and a monocolonal antibody that specifically binds to the synthetic and polypeptide and a carrier; and a monocolonal antibody that specifically binds to the synthetic and a carrier; and apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal cuch mapper serum cholesterol in a subject (including a mammal chimperse or orangutan); for treating occomary artery disease, chimpanzee or orangutan); for treating occomary artery disease, chypetalipoprotein and anterosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; my and also for treating and; an atterosclerosis; and colipoprotein (UDD) or very low density lipoprotein (VDD) to a cell and enhances degradation of LDD or very low density lipoprotein. This sequence represents a synthetic apolipoprotein-E
(including animal or plant) comprising the synthetic apolipoprotein-E
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100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 6.4e-08; tive 0; Mismatches 0; Indels 1 GIRRFLGSIWRFIRAFYG 18 Query Match
Best Local Similarity 100.
Matches 18; Conservative 셤

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Gaps ö

ADO34236 standard; peptide; 18 AA. ADO34236;

12-AUG-2004 (first entry)

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 13.

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; servoke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

Synthetic.

WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P.

(UABR-) UAB RES FOUND

Anantharamiah GM, Garber DW, Datta G;

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 13; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E RESULT 4
AD034236
ID AD034236
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c mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and a monocolonal antibody that specifically binds to the synthetic and a polipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide antiarteriosclerotic, cerebroprotective, and cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and cardiant, vasotropic, antiarteriosclerotic, mimicking polypeptide is cusquil for reducing serum cholesterol in a subject (including a mammal cusquil for reducing serum cholesterol in a subject (including a mammal cultimaginal). For treating occonary artery disease, dysbetalipoproteinsemia or troke; for breaking an embolus in the subject; dysbetalipoproteinemia or troke; for breaking an embolus in the subject; colypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL;
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 AA;
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the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, app. the manner or cangutan); for treating coronary artery disease, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for treating coronary and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide chances binding of low-density lipoprotein (UDL) or a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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       Score 98; DB 8; Length 18; Pred. No. 6.4e-08;
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Query Match
Best Local Similarity 100.
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Gaps

1 GIRRFLGSIWRFIRAFYG 18

RESULT 6 ADO34314

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Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 91. ADO34314 standard; peptide; 18 (first entry) 12-AUG-2004 AD034314; 

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction, stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

Synthetic

WO2004043403-A2.

27-MAY-2004

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND.

Datta G; Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 91; 79pp; English

The invention relates to a novel synthetic apolipoprotein-E mimicking polygeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypeptide acomposition comprising the synthetic apolipoprotein-E mimicking polypeptide and a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic

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an monoclonal antibody that specifically binds to the synthetic
apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
mimicking polypeptide has the following activities: antilipaemic,
cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
useful for reducing serum cholesterol in a subject (including a mammal
companzee or orangutan); for treating coronary artery disease,
chimpanzee or orangutan; for treating coronary artery disease,
compocardial infarction or stroke; for breaking an embolus in the subject;
myocardial infarction or stroke; for breaking an embolus in the subject;
condition and an entroperior (UDL) or very low
density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
controlled to the controlle
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
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mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein. E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinnemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein. E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VDD) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein. E mimicking polypeptide of the invention.

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mumicking polypeptide has the following activities: antiliperic cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteineamia or atheroclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 94; DB 8; Length 18;
Pred. No. 2.6e-07;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADO34338 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity 88.99

Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                             Sequence 18 AA;
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Gaps

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0; Indels

95.9%; Score 94; DB 8; Length 18; 88.9%; Pred. No. 2.6e-07;

2; Mismatches

16; Conservative

Matches

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Query Match Best Local Similarity

Sequence 18 AA;

18 18

1 GIRRFLGSIWRFIRAFYG

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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E apolipoprotein-E
                                                                                                                                                     vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; siroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis
                                                                                                                                    apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; SEQ ID NO 115; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Datta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprises an amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anantharamiah GM, Garber DW,
                                                                                                                                                                                                                                                                                                                                                         13-NOV-2003; 2003WO-US036268
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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
                                                                                                                                                                                   apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina: low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
                                                                                                                                                 Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 129.
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                                    ADO34352 standard; peptide; 18 AA
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                                                                                                              12-AUG-2004 (first entry)
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                                                                                                                                                                                                                                                                                                            Synthetic
                                                                          ADO34352;
RESULT 9
                    AD034352
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antianginal. The synthetic apollopprotein-E minicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E minicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density, lipoprotein (LDL) to a cell and enhances degradation of LDL or wiminicking polypeptide of the invention.
  vasotropic, antiarteriosclerotic, cerebroprotective, and
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Gaps
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95.9%; Score 94; DB 8; Length 18; 88.9%; Pred. No. 2.6e-07; Mismatches 0; Indels
                                                           1 GIRRFLGSIWRFIRAFYG 18
                                                                                   18
                                                                                  1 GIRRFLGSLWRFLRAFYG
                    Local Similarity 88.5
           Query Match
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Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117. ADO34340 standard; peptide; 18 AA (first entry) 12-AUG-2004 ADO34340; RESULT 10 

apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholestron; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDL;

Synthetic.

WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268.

(UABR-) UAB RES FOUND.

ö Datta Anantharamiah GM, Garber DW, WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 117; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypuclectide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic and apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide, and activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and a monoclonal antibody that specifically binds to the synthetic anolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide and a carrier; and apolipoprotein-E mimicking polypeptide and activities; antilipaemic, cardiant, vasotropic, antiateriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis

Claim 4; SEQ ID NO 116; 79pp; English.

comprises an amino acid sequence

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          useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating ocronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (ULD) to very low density lipoprotein (VLD) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholestreol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina: low-density lipoprotein; LDL; very low density lipoprotein; UDL).
antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116.
                                                                                                                                                                                   Score 94; DB 8; Lengtn 10;
Pred. No. 2.6e-07;
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                                                                                                                                                                                                  95.9%;
88.9%;
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                                                                                                                                                                                                                                                                        12-AUG-2004 (first entry)
                                                                                                                                                                                                               Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                       Sequence 18 AA;
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                   such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, rat dysbetaliapproteinsemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking density lipoprotein (UDI) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein of LDL or mimicking mimicking polypeptide of the invention.
for reducing serum cholesterol in a subject (including a mammal
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Gaps
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0
Length 18
                         0; Indels
95.9%; Score 94; DB 8; 1
88.9%; Pred. No. 2.6e-07;
                       2; Mismatches
                                                  1 GIRRFLGSIWRFIRAFYG 18
             Local Similarity 88.9
nes 16; Conservative
  Query Match
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GLRRFIGSIWRFIRAFYG 18

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Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 74.
    ADO34297 standard; peptide; 18 AA
               12-AUG-2004 (first entry)
          AD034297;
RESULT 12
  AD034297
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apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDDL.

Synthetic

WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

ö Datta Anantharamiah GM, Garber DW,

WPI, 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 74; 79pp; English

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide and activities: antilipeamic, cardiant, vasotropic, antiarteriosoleroric, cerebroprotective, and antiandinal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-B mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E amimicking polypeptide. The synthetic apolipoprotein-E cardiant, vasotropic, antiatreciosclerotic, cerebroprotective, and antiandinal. The synthetic apolipoprotein-E mimicking polypeptide is subject in a subject (including a mammal antianding serum cholesterol in a subject (including a mammal

such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

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    chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (UDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                          apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis
                                                                                                                                                                                                Gaps
rat, rabbit, cow, sheep, pig, human, monkey, ape,
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                                                                                                                                                                Score 92, DB 8; Length 18;
Pred. No. 5.3e-07;
2; Mismatches 0; Indels
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                                                                                                                                                                     93.9%;
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                                                                                                                                          Sequence 18 AA;
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antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

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chimpanzee or orangutan); for treating coronary artery disease, despetablishments or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypepticle enhances binding of low-density lipoprotein (IDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
                                                                                                                                                                                                                                                                                                                                                                                                                       apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
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                                                                                                                                                       Length 18;
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                                                                                                                                                    93.9%; Score 92; DB 8; Le
88.9%; Pred. No. 5.3e-07;
iive 2; Mismatches 0;
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                                                                                              mimicking polypeptide of the invention
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                                                                                                                                                                                                             1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                           Sequence 18 AA;
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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic and apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antlarteriosclerotic, cerebroprotective, and

Claim 4; SEQ ID NO 53; 79pp; English

comprises an amino acid sequence.

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             useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, himpanzee or orangutan); for treating ocronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke, for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking oblypeptide enhances binding of low-density lipoprotein (ULD) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and a monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiateriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL; very low density lipoprotein; UDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic apolipoprotein-E mimicking related R18L linear peptide.
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                                                                                                                                                                                                                                                                                                 Score 92; DB 8; Length 18; Pred. No. 5.3e-07; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADO34227 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   18
                                                                                                                                                                                                                                                                                                                                                                                          1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garber DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-NOV-2003; 2003WO-US036268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-NOV-2002; 2002US-0425821P.
                                                                                                                                                                                                                                                                                                      93.98;
                                                                                                                                                                                                                                                                                                                        88.98;
                                                                                                                                                                                                                                                                                                                                                                                                                   1 GIKRFLGSIWRFIKAFYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                        Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004043403-A2
                                                                                                                                                                                                                                                             Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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                                                                                                                                                                                                                                                                                                        Query Match
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ADO34227
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useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape; dyshetalipoproteinaemis or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein. E mimicking obytypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein. E mimicking mimicking polypeptide of the invention.
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ö Gaps ; 0 Query Match
Best Local Similarity 94.4%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 1; Indels

ઠે a Search completed: May 19, 2006, 14:24:30 Job time : 94.2857 sec8

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

May 19, 2006, 14:24:57 ; Search time 14.2857 Seconds (without alignments) 121.233 Million cell updates/sec Run on:

US-10-712-447-2 98 Title: Perfect score:

1 GIRRFLGSIWRFIRAFYG 18 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_80:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	hypothetical prote	transcription regu	2-oxoglutarate/mal	poly (3-hydroxybuty	leucyl-tRNA synthe	leucine-tRNA ligas	acriflavin resista	hypothetical prote	О	hetical pr	NIP1 protein - yea	TMV resistance pro	reverse transcript	penicillin-binding	F	-	hypothetical prote	hypothetical prote		o-antigen export s	o-antigen export s		lass I	HLA-A-0	class I	class I	class I hi	ဗ	gene HLA-A-0205 pr
	Ω	S76462	A75578	G64537	A34341	A84060	H64102	AH3568	T32316	B84733	T33269	A46417	T04583	T12085	584953	T52113	D72540	T15530	B72692	I54412	F71707	D97700	HTHM69	HLHUA2	I38443	161902	137542	8444	9	I38442
	DB	i i	~	٦	~	~	7	~	7	7	~	~	~	~	~	~	~	~	~	~	7	~						~		
	Query Match Length	627	178	461	589	806	861	1025	265	489	516	812	1607	407	760	107	214	228	237	246	258	258	273	365	365	365	365	365	365	365
de	Query Match	49.0	45.9	44.9	44.9	4.	44.9	44.4	43.9	43.9		43.9	43.9	43.4	43.4	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	•	42.9	42.9	42.9
	Score	48	45	44	44	44	44	43.5	4	43	43	43	43	42.5		4	42	42	42	42	42	42	42	42	42	42	42	42	42	42
	Result No.	1	7	m	4	S	9	7	80	đ	10	11	12	13	14	15	16		18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote leucyl-tRNA synthe	leucyl-tRNA Bynthe leucyl-rRNA Bynthe	leucine-tRNA 11gas homolog to drosoph	hypothetical prote vfap protein - Rac	dimethylbulfoxide	hypothetical prote	probable permease	hypothetical prote	hypothetical prote	hypothetical prote	cytochrome P450 DW
T04745 AD1282	AH1653 B89961	D69650 T50337	AG2115	C42333 E64109	T20575	AF2599 G97381	T08940	F96571	D96776	T02263
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537 803	803 804	804 790	131	279	359	364 364	384	406	503	519
42.9 6.59	42.9 42.9					41.8 41.8	41.8	41.8	41.8	41.8
4 4 2 2	4 4 2 2	42	41	4 4 1 1	41	41	41	41	41	41
30 31	332	3.4 5.5	36	38	39	4 4 0 1	42	43	44	45

## ALIGNMENTS

W.Reference.number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76462
A;Status: preliminary
A;Aolecule type: DAN
A;Residues: 1-627 kMN
A;Residues: 1-627 kMN
A;Cross-references: UNIPROT:P74489; UNIPARC:UPI00000C103F; EMBL:D90915; GB:AB001339; NID:A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 "Species: Synechocystis sp.
A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004
C; Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 05-Jul-2004
D; R; Doumura, S; Shimpo, S; Takeuchi, C; Wada, T; Watanabe, A; Yamada, M; Yasuda, D; R; Diagnost analysis of the genome of the unicellular cyanobacterium Synechocystis ö Gaps ö 49.0%; Score 48; DB 2; Length 627; 38.9%; Pred. No. 8.1; tive 6; Mismatches 5; Indels hypothetical protein - Synechocystis sp. (strain PCC 6803) |::|| ||::| 597 GLEQLLGKIWQWLRQKFG 614 1 GIRRFLGSIWRFIRAFYG 18 Query Match Best Local Similarity 38.99 Matches 7; Conservative RESULT 1 ò 셤

Liangeription regulator, Mark family - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004
C;Accession: A75578
C;Accession: A75578
C;Accession: A75578
C;Accession: A7578
C;Accession: A7578
C;Accession: A7578
C;Accession: A7579
C;Accession: A7579
C;Accession: A75578
C;Accession: A7

C;Genetics: A;Gene: DRA0248

Query Match

45.9%; Score 45; DB 2; Length 178;

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acriflavin resistance protein F [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AH368
R;DelVacchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, h.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesse
                                                                                                                                                                                                                                                         R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maeui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and ç
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-806 <STO>
A;Cross-references: UNIPROT:Q9K7S8; UNIPARC:UPI0000136555; GB:AP001518; GB:BA000004; NID:
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: UNIPROT:P43827; UNIPARC:UP1000013655F; GB:U32774; GB:L42023; NID:g15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rifleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, i Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 259, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
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                                                                                                                                            leucyl-tRNA synthetase leuS [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec.2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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C,Superfamily: leucine-tRNA ligase
C,Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-861 <TIGR>
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Pred. No. 48;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 806;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
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Pred. No.
100 RRFAGDAWRTNLPYRFAAAFY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C'Genetics:
A'Gene: leuS
C;Superfamily: leucine-tRNA ligase
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Similarity 53.8%;
7; Conservative
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665 GAKRFLGRVWNLV 677
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Matches 6; Conservative
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                         C;Species: Helicobacter pylori
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: G64537
C;Accession: G64537
C;Accession: G.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne Onn, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, S39-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Peoples, O.P.; Sinskey, A.J.
V. Biol. Chem. 264, 15298-15303, 1989
A;Title: Chem. 264, Vidroxybutyrate (FHB) biosynthesis in Alcaligenes eutrophus H16. Iden
A;Reference number: A34341; MUID:89359357; PMID:2670936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynt
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A;Note: the authors translated the codon TAC for residue 120 as Thr
C;Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:g141958; PIDN:
A;Experimental source: strain H16
R;Schubert, P.; Krueger, N.; Steinbuechel, A.
J. Bacteriol. 173, 168-175, 1991
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                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                            2-oxoglutarate/malate translocator - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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A,Residues: 1-461 - 4TOM>
A)Cross-references: UNLPARC:UPI0000174217; GB:AE000511; TIGR:HP0143
C,Superfamily: 2-oxoglutarate/malate translocator
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44.9%; Score 44; DB 2; Length 589;
Best Local Similarity 47.6%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 461;
                                   Indels
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                                      4
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Pred. No. 26;
2; Mismatches
Pred. No. 7.2;
0; Mismatches
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53.8%;
   69.2%;
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297 VRRLLSWFWRFVR 309
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                                                                                            2 IRRFLGSIWRFIR 14
                                                                                                                                                      23 ILRFLGGIWRLNR 35
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Best Local Similarity 53.8
Matches 7; Conservative
                                   9; Conservative
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Best Local Similarity
Matches 9; Conserv
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A;Molecule type: DNA
A;Residues: 1-589 <PEO>
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A; Status: preliminary
A; Molecule type: DNA
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A; Accession: A34341

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NIPI protein - yeast (Saccharomyces cerevisiae)
NiAlternate names: nuclear import protein; protein YM9924.01c; protein YM9952.11c; protei)
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: 21-Sep-1993 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A46417; S53979; S53902
R;Gu, Z.; Moerschell, R.P.; Sherman, F.; Goldfarb, D.S.
Proc. Natl. Acad. Sci. U.S.A. 89, 10355-10359, 1992
A;Title: NIPI, a gene required for nuclear transport in yeast.
A;Reference number: A46417;
A;Accession: A46417
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A,Residues: 1-110,'v',112-582,'Q',584-602 <CHU>
A).Cross-references: UNIPARC:UPIO000168ACA; EMBL:Z54141; NID:g1072408; PID:g984682; MIPS:)
A;Experimental source: strain AB972
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A;Molecule type: DNA
A;Residues: 571-582,'Q',584-640,'K',642,'K',644-812 <CON>
A;Cross-references: UNIPARC:UP10000168ACD; EMBL:Z49212; NID:g798940; PID:g798951; MIPS:YN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:076442; UNIPARC:UPI000007D477; EMBL:AF068709; PIDN:AAC19257.1
A;Experimental source: strain Bristol N2; clone C24B9
                        P450 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
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A;Cross-references: UNIPROT:P32497; UNIPARC:UPI000017B2E1; EMBL:L02899
A;Note: sequence extracted from NCBI backbone (NCBIN:117849, NCBIP:117850)
R;Connor, R; Churcher, C.M.
asubmitted to the EMBL Data Library, April 1995
A;Reference number: S53969
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A;Map position: 2
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome
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                                                                                Length 489
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                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C24B9.13 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: T33269
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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43.9%; Score 43; DB 2;
Best Local Similarity 41.2%; Pred. No. 42;
Matches 7; Conservative 5; Mismatches
                                                                                Score 43; DB 2;
Pred. No. 40;
4; Mismatches
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submitted to the EMBL Data Library, September 1995
A, Reference number: S59302
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A;Map position: 5
A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2
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                                                                                Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
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54 IGNMWSFLRAF
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A; Residues: 1-812 <GU1>
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A.Reference number: A84420; MuID:20083487; PMID:10617197
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                           A,Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A,Reference number: AD3252, PMID:11756688
                                                                                                                              A;Molecule type: DNA
A;Residues: 1-1025 «KUR»
A;Cross-references: UNIPROT:Q8YCQ5; UNIPARC:UP10000584C8; GB:AE008918; PIDN:AAL53715.1;
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:017136; UNIPARC:UP1000007D19A; EMBL:AF024503; PIDN:AAB70384. A;Experimental source: strain Bristol N2; clone F31F4
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
C;Accession: T32316
R;Blanchard, M.; Kamer, J.; Elliott, G.; Twyman, B.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F31F4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A;Introns: 13/3; 67/2
C;Superfamily: Caenorhabditis elegans hypothetical protein T09F5.1
                                                                                                                                                                                                                                                                                                                                                                                                            44.4%; Score 43.5; DB 2; Length 1025; 50.0%; Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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A;Molecule type: DNA
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Pred. No. 22;
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   Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
                                                                                                                                                                                                                                                                                                                            A;Map position: II
C;Superfamily: hypothetical protein b2075
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531 FLGSVWSFMTLPRSFF 546
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53.8%;
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Best Local Similarity
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Matches 8; Conserv
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A;Molecule type: DNA
A;Residues: 1-489 <STO>
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                                                                                                                        A;Status: preliminary
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Search completed: May 19, 2006, 14:39:56 Job time : 14.2857 secs
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178 GIRSFLGHVGFYRRFIRDF 196
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Similarity 44.4%;
8; Conservative
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A,Map position: V
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T52113
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A;Molecule 19683
A;Accession: T04583
A;Accession: DABA
A;Residues: 1-1607 ABEV>
A;Cross-references: UNIPROT:O65506; UNIPARC:UPI00000AA45C; EMBL:AL022141
A;Rexperimental source: cultivar Columbia; BAC clone F23E13
B;Bevan, M:; Wedler, H:; Wambutt, R:; Hoheisel, J:; Wewes, H:W.; Mayer, K.F.X.; Schuelle submitted to the Protein Sequence Database, April 1998
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                                                                                                                                                                                                                                                                                                                                                                         TWV resistance protein N homolog F23E13.30 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C;Accession: T04583; T05507 T85807 R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse, submitted to the Protein Sequence Database, March 1998 A;Reference number: 215378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T12085
R;Kinoshita, T.; Wada, H.; Masaaki, I.; Shimazaki, K.
submitted to the EMBL Data Library, September 1997
A;Description: Retrotransposon-like cDNAs from guard cell protoplasts in Vicia faba.
A;Reference number: Z17406
A;Accession: T12085
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C;Species: Vicia faba (fava bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.9%; Score 43; DB 2; Length 1607; ilarity 72.7%; Pred. No. 1.3e+02; Conservative 0; Mismatches 3; Indels
                                                                                                                           2; Length 812;
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                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: T05507
A;Molecule type: DNA
A;Residues: 1448-1607 <BE2>
A;Cross-references: UNIPARC:UPI000016DBFD; EMBL:AL022373
A;Experimental source: cultivar Columbia; BAC clone T19K4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4,
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A;Introns: 193/2; 238/2; 556/2; 930/3; 1029/3; 1287/3
A;Note: F23E13.30; T19K4.270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-407 <KIN>
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43.4%; Score 42.5; Di
Best Local Similarity 57.9%; Pred. No. 40;
Matches 11; Conservative 1; Mismatches
                                                                                                                        Score 43; DB
Pred. No. 66;
                                                                                                                                                                        4; Mismatches
                    A,Gene: SGD:NIP1
A,Crose-references: SGD:S0004926; MIPS:YMR309c
A,Map position: 13R
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                                                                                                                      Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                     361 GVKRILGSIFSFV 373
                                                                                                                                                                                                                       1 GIRRFLGSIWRFI 13
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Best Local Similarity
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     C; Genetics:
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probable transcription co-activator KIWI [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52113
A;Title: Isolation of putative plant transcriptional coactivators using a modified two-hy A;Reference number: 225848; MUID:98346011; PMID:9681033
A;Accession: T52113
A;Accession: T52113
A;Accession: T52113
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-107 < COR>
A;Residues: UNIPROT:O65154; UNIPARC:UP1000000C45F; EMBL:AF053302; PIDN:AAC08574.1
                                   C;Species: Buchnera sp.
C;Daces: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Accession: E84953
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. Al
A;Title: Genome sequence of the endocellular pacterial symbiont of aphids Buchnera sp. Al
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                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Wolecule type: DNA
A;Residues: 1-760 <STO>
A;Cross-references: UNIPARC:UPI000005E4C8; GB:AP000398; GSPDB:GN00144
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penicillin-binding protein 1b (imported) - Buchnera sp. (strain APS)
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42.9%; Score 42; DB 2;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 42.5; DE; Pred. No. 74; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: penicillin-binding protein 1B
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

May 19, 2006, 14:13:32 ; Search time 115.429 Seconds (without alignments) 144.247 Million cell updates/sec Run on:

US-10-712-447-2 98 Title: Perfect score:

1 GIRRFLGSIWRFIRAFYG 18 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2849598 Total number of hits satisfying chosen parameters:

2849598 segs, 925015592 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: uniprot\_sprot:\* 2: uniprot\_trembl:\* UniProt\_7.2:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

0>C 2007007		· 6	
05gh40 brachydanio 05gh77 rattus norv 05gh73 homo sapien 08kby2 chlorobium 02y8v4 nitrosospir 03xw00 magnetococc 05g415 salinibacte 05cp27 cryptospori 05ryr0 delnococcus 06llt5 picrophilus 04b881 burkholderi 07vv93 bordetella 07w7p3 bordetella	ae; , Glavina T., Larimer F.,	5; 0; Gaps	gota; vrnia;
<u> </u>	H PRELIMINARY; PRT; 805 AA.  integrated into UniProtKB/TrEMBL.  sequence version 1.  entry version 1.  sequence class Ia (EC 6.1.1.4).  sontheres class Ia (EC 6.1.1.4).  chlorochromatil (strain CaD3).  chlorochromatil (strain CaD3).  chlorochromatil (chrombiales; Chlorobiaceae; Pelodictyon group; Chlorobiales; Chlorochromatii CaD3."; Larime; Capides N.; Panonova, N.; Richardson P.; Chlorobiales; Chlorochromatii CaD3."; AUG-2005) to the EMBL/GenBank/DDBJ databases.  by the UniProt Consortium, see http://www.uniprot.orunder the Creative Commons Attribution-Noberivs Lic.  108; ABS28940.1; -: Genomic_DNA.  524; F:ATP binding; IEA.  872; F:Leucyl-tRNA aminoacylation; IEA.  873; F:Leucyl-tRNA aminoacylation; IEA.  874; F:Ligase activity; IEA.  875; F:Leucyl-tRNA aminoacylation; IEA.  876; P:Ligase activity; Chlorobiales (Profeome; Ligase.)  877; P:Ligase activity; Chlorobiales (Profeome; Ligase.)  878; P:Ligase activity; Chlorobiales; Chlorobiale	;; Length 805	RELIMINARY; PRT; 670 AA. egrated into UniProtKB/TrEMBL. uence version 1. ry version 25. il (Fragment). emlineata (Colorado potato beetle). emlineata (Colorado Potato beetle). emlineata (Colorado Potato beetle).
OSCH40_BRARE XKR6_RAT XKR6_HUMAN XKR6_HUMAN SYL_CHLIFE Q2X804 DIRMU Q3XW00_9PROT Q28415_9SPHI Q5CP27_CKYPV Q8KYR0_DEIRA Q6L015_PICTO Q4CSBI BURVI Q7WY93_BORPE Q7W7P3_BORPE Q7W7P3_BORPE Q7W7P3_BORPE	CHICH  QJAPYS_CHICH  PRELIMINARY; PRT; 805 AA.  QJAPYS_;  22-NOV-2005, integrated into UniProtKB/TrEMBL.  22-NOV-2005, sequence version 1.  21-EBE-2006, entry version 5.  21-EBE-2006, entry version 5.  Chorobium chlorochromatii (strain CaD3).  OrderedLocusNames=Cag_1688;  Chlorobium/Pelodictyon group; Chlorobium.  NCHI TaxID=34017;  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  US DGE Joint Genome Institute;  COMPOLED SEQUENCE [LARGE SCALE GENOMIC DNA].  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  US DGE Joint Genome Institute;  COMPOLED SEQUENCE (LARGE CADE GENOMIC DNA].  Land M., Kyrpides N., Ivanova N., Richardson P.;  Land M., Kyrpides N., Ivanova N., Richardson P.;  Compolete Sequence of Chlorobium chlorochromatii (caD3)  Submitted (AUG-2005) to the EMBL/GenBank/DDBJ database  Copyrighted by the Uniprot Consortium, see http://www.  Copyrighted under the Creative Commons Attribution-Nol  Distributed under the Creative Commons Attribution-Nol  Distributed under the Creative Commons Attribution-Nol  GO; GO:0006524; F:ATP binding; IEA.  GO; GO:0006524; F:ATP binding; IEA.  GO; GO:0006429; F:leucine-tRNA ligase activity; IEA.  GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.  Aminoacyl-tRNA synthetess; Complete sproteome; Ligase.  Aminoacyl-tRNA synthetesse; Complete sproteome; Ligase.  Application of the Complete Sproteome; Ligase.  GO:000429; P:ATP Dinding; IEA.	core 58; DB 2 red. No. 3.2; Mismatches	PRELIMINARY; PRT; 670 AA. integrated into UniProtKB/TrEMBL. sequence version 1. entry version 25. ein 1 (Fragment). decemlineata (Colorado potato beetle) tazoa; Arthropoda; Hexapoda; Insecta;
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580 638 6411 837 853 853 248 218 218 278 278 278 278	RELIMINA ggrated lence ve versi vy versi v	h 59 Similarity 69 9; Conservative 1 GIRRFLGSIMRFI 3 	DE PRELIMINARY;  6, integrated into U 6, sequence version 6, entry version 25.  rotein 1 (Fragment).  sa decemlineata (Col Metazoa; Arthropoda
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<b>ፋፋፋፋፋፋፋፋፋፋፋ</b> የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ	H	mil O IRR ISR	DE 6, 6, rot me End
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₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩	RESULT 222 PT 22	Ouery Dest Language Matche	RESULT 10 25271 10 000 10 0000 10 000 10 000 10 000 10 000 10 000 10 000 10 000 10 000 10 000

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GO; GO:0015031; P:protein transport; IEA.
GO; GO:006508; P:proteolysis; IEA.
InterPro; IPR01527; ABG TW 1.
InterPro; IPR011527; ABG TW 1.
InterPro; IPR011527; ABG TW transpt.
InterPro; IPR00140; ABG TW transpt.
InterPro; IPR005043; ABG TW transpt.
InterPro; IPR005043; Peptidase C39.
InterPro; IPR0132; Type I sec HlyB.
PANTHER; PTHN19242:SFT4; Type I sec HlyB; I.
Pfam; PP00664; ABC membrane; I.
Pfam; PP00065; ABC tran; I.
Pfam; PP00006; ABC tran; I.
Prodom; P0000006; ABC transporter; I.
Prodom; P000006; ABC transporter; I.
PROSITE; PS0021; ABC TRANSPORTER; I.
PROSITE; PS00221; ABC TRANSPORTER; I.
PROSITE; PS00221; ABC TRANSPORTER; I.
PROSITE; PS00291; ABC TRANSPORTER; I.
PROSITE; PS00909; PEPTIDASE C39; I.
PROSITE; PS00909; PEPTIDASE C39; I.
PROSITE; PS00909; PEPTIDASE C39; I.
PROSITE; PS00900; PEPTIDASE C39; I.
PROSITE; PS00900; PEPTIDASE C39; I.
PROSITE; PS00900; PEPTIDASE C39; I.
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Q44QD1;
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016887; F:ATPase activity; coupled to transmembrane m. . .; IEA.
GO; GO:000166; F:MITPase activity; coupled to transmembrane m. . .; IEA.
GO; GO:0000166; F:Inucleactide binding; IEA.
GO; GO:00001823; F:peptidase activity; IEA.
GO; GO:000855; F:protein transporter activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                 de Kort C.A.D., Koopmanschap A.B.; "Nucleotide and deduced amino acid sequence of a cDNA clone encoding diapause protein 1, an amylphorin-type storage hexamer of the Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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MEDLINE-21360352; PubMed=11467725; DOI=10.1139/cjm-47-6-495;
Venter A.P., Twelker S., Oresnik I.J., Hynes M.F.;
"Analysis of the genetic region encoding a novel rhizobiocin from Rhizobium leguminosarum bv. viciae strain 305.";
Can. J. Microbiol. 47:495-502(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 55.1%; Score 54; DB 2; Length 670; Best Local Similarity 43.8%; Pred. No. 11; Matches 7; Conservative 6; Mismatches 3; Indels
            Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 670 AA; 79825 MW; 8A000BA115BEC8A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                GO, GO:0005344; F:oxygen transporter activity; IEA. GO; GO:0006810; P:transport; IEA. InterPro; IPR000896; Hemcoyanin. InterPro; IPR005203; hemcoyanin. C. InterPro; IPR005204; hemcoyanin. C. InterPro; IPR005204; hemcoyanin. C. InterPro; IPR01511; Hemcoyanin, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001, integrated into UniProtKB/TrEMBL
01-MAR-2001, sequence version 1.
07-FEB-2006, entry version 25.
ABC transporter RzcB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      735 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF273216; AAG25076.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF03723; Hemocyanin_C; 1.
Pfam; PF00372; Hemocyanin_M; 1.
Pfam; PF03722; Hemocyanin_N; 1.
PRINTS; PR0187; HAEMOCYANIN_2; UNKNOWN_1.
                                                                                                                                                                                                                              J. Insect Physiol. 40:527-535(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 RHILV
Q9F7V7 RHILV PRELIMINARY; PRT;
Q9F7V7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhizobium leguminosarum bv. viciae.
                                                                                                                                                                                                                                                                                                                                                   EMBL; X76080; CAA53691.1; -; mRNA.
HSSP; P04253; 1LL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:| |::| ::| |:|
351 RKFYGALWSYLRHFFG 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RRFLGSIWRFIRAFYG 18
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                                                                                                            NUCLEOTIDE SEQUENCE
                                     Leptinotarsa.
NCBI_TaxID=7539;
                                                                                                                                                                                                          potato beetle.
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SEQUENCE
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Q9F7V7 RH
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Chlorobium limicola DSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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13-5E2-2005, sequence version 1.
13-5E2-2005, entry version 9.
1-EB2-2006, entry vers
                                                                                                                   Length 735;
                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
80717 MW; 0216259241F3630C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AAHJO1000009; EAM43320.1; -; Genomic_DNA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
GO; GO:000429; F:leucyl-tRNA aminoacylation; IEA.
InterPro; IPR002302; Leu tRNAByn_la.
Pfam; PF00133; tRNA-synt_l; 1.
                                                                                                                   Score 52; DB 2;
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  805 AA.
                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 GFRWFLPAIWRYRRAF 176
                                                                                                                          53.1%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                               1 GIRRFLGSIWRFIRAF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                    Local Similarity 62.5
nes 10; Conservative
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STRAIN=DSM 245;
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SKRDR

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                                                       22-NOV-2005, sequence version 1.
21-FEB-2006, entry version 4.
Hypothetical protein.
Order-edLocusNames=Escep18194 A3207;
Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760)
/ NCIB 9086 / R18194))
                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
US DOE Joint Genome Institute;
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
Hammon N., Israni S., Fuluck S., Chain P., Malfatti S., Shin M.,
Vergez L., Schmutz J., Larimer F., Land M., Kyrpides N., Lykidis A.,
                                                                                                                                                                 Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, Burkholderia, Burkholderia cepacia complex.
                                                                                                                                                                                                                                                                                                                                                        "Complete sequence of chromosome 1 of Burkholderia sp. 383.";
Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; CP000151; ABB06809.1; -; Genomic_DNA.
Complete protecme; Hypothetical protein.
SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51; DB 2;
Pred. No. 20;
039L57_BURS3 PRELIMINARY; PRT; 407 AA. 039L57; 010V-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GIRRFLGSIWRFIRAFY 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 52.0%;
Local Similarity 47.1%;
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary data.
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                                                                                                                                                                                                        NCBI_TaxID=269483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=AU 1054;
                                                                                                                                                                                                                                                                                                                                            Richardson P.;
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                       Gaps
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Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Chlorobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlorobium phaeobacteroides DSM 266.
Bacteria, Chlorobi, Chlorobia, Chlorobiales, Chlorobiaceae;
Chlorobium/Pelodictyon group; Chlorobium.
                                                                                              Score 52; DB 2; Length 805;
Pred. No. 29;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2005, sequence version 1.
21-F8B-2006, entry version 9.
Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
ORFNames-Cpha266DRAFT_2546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phaeobacteroides DSM 266.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AAIB01000002; EAM35935.1; -; Genomic_DNA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
GO; GO:0006429; F:leucine-tRNA minoacylation; IEA.
InterPro; IPR002302; Leu tRNAByn_la.
Fam; PF00133; tRNA-synt_l; 1.
PRINTS; PR00395; TRNASYNTHIEU.
TIGRFAM; TIGRO396; leus_bact; 1.
Aminoacyl-tRNA synthetase.
SEQUENCE 816 AA; 93335 MW; 6770BIDAC50560F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=DSM 266;
US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Chlorobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       816 AA; 93335 MW; 6770B1DAC50560F1 CRC64;
                         TIGREAMS; TIGR00396; leus_bact; 1.
Aminoacyl-tRNA synthetase.
SEQUENCE 805 AA; 91997 MW; D4F3FE28F9E92DF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.1%; Score 52; DB 2;
61.5%; Pred. No. 29;
ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                13-SEP-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                             816 AA.
                                                                                                                                                                                                                                                                                                             PRT;
       PRINTS; PR00985; TRNASYNTHLEU
                                                                                                  Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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622 GISRFLGKVWRLV 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phaeobacteroides DSM 266."
                                                                                                                                                                                                                  622 GISRFLGKVWRLV 634
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                                                                                                                                                                             1 GIRRFLGSIWRFI 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=290317;
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                                                                                                                                                                                                                                                                                                             Q43K01 9CHLB
Q43K01;
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Gaps

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Length 407; 4; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequencing of the draft genome assembly of Burkholderia cenocepacia AU 1054.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=AU 1054;
US DOB Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US DOE Joint Genome Institute (JGI-PQF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
                                                                                                                                                                                                                OŘFNames=BcenDRAFT_3751;
Burkholderia cenocepacia Bu 1054.
Bacteria; Proteobacteria Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU 1054.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
0456F4 9BURK PRELIMINARY; PRT; 408 AA. 0456F4; 13-SEP-2005, integrated into UniProtKB/TrEMBL. 13-SEP-2005, sequence version 1. 07-FEB-2006, entry version 2. Hypothetical protein.
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Q39L57\_BURS3

RESULT 6

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Name=XKR7; Synonyms=C20orf159, XRG7;
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109
280
334
375
404
            Homo sapiens (Human).
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nes 7; Conserv
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355
384
415
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Best Local 8
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                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                               US DOE Joint Genome Institute (JGI-FGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pilluck S., Richardson P.,
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Larimer F., Land M., "Annotation of Burkholderia cenocepacia
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
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                                                                                                                                                                                                                                                                Burkholderia cenocepacia H12424.
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, Burkholderia, Burkholderia cepacia complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 52.0%; Score 51; DB 2; Length 408; Best Local Similarity 47.1%; Pred. No. 20; Matches 8; Conservative 5; Mismatches 4; Indels
                                                                52.0%; Score 51; DB 2; Length 408; 47.1%; Pred. No. 20; ative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt H12424."}_j Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                 Hypothetical protein.
SEQUENCE 408 AA; 45545 MW; 3C2BCA9471BAAE93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ll protein.
408 AA; 45603 MW; 7F39388B305911D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XKR7 HUMAN STANDARD; PRT; 579 AA. QSGH72; Q9NUG5; 11-OCT-2005, integrated into UniProtKB/Swiss-Prot. 01-MAR-2005, sequence version 1. 07-FEB-2006, entry version 8. XK-related protein 7.
                     EMBL; AAHI01000010; EAM12352.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AAHL01000063; EAM16412.1; -; Genomic_DNA.
                                                                                                                                                                                      Q4LK44 9BURK PRELIMINARY; PRT; 408 AA. Q4LK44; 02-AUG-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=H12424;
US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                      02-AUG-2005, sequence version 1. 07-FEB-2006, entry version 2. Hypothetical protein.
                                                                                                                          |||: || :|:: |: |
328 GIRQMLGHVWQWTRSSY 344
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                                                                                                            1 GIRRFLGSIWRFIRAFY 17
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                                                                                                                                                                                                                                                        ORFNames=Bcen2424DRAFT 1071;
                                                                         Local Similarity 47.1
                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=331272;
                                                                                                                                                                                                                                                                                                                                    STRAIN=HI2424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
                                                                 Query Match
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REPUINES-GROUED ESCOUENCE [LARGE SCALE GENOMIC DNA].

RA WEDLINES-G18349; bubMed=11780052, DOI=10.1038/414865a;

RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Balley J., Barlow K.F., Bartes K.N., Barden M.M.,

RA Basley O.P., Bird C.P., Blakey S.E., Baridgeman A.M., Brown A.J.,

RA Baniey J., Bird C.P., Blakey S.E., Carder C., Carter N.P.,

RA Clegs S., Cobley V.E., Collier R.E., Cornor R.E., Corby N.R.,

Clegs S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

RA Clington A., Crankland J.A., Fraser A., French L., Garrer P.,

RA Stalington A.G., Frankland J.A., Fraser A., Brench L., Garrer P.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA RAP, Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

Lehvaeslaino M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

Mine S.A., Mistry D., Moconachie L.J., McLay K., McMarray R.A.,

RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sins S.,

Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,

Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,

RA Tracey A., Tromans A.C., Vaudin M., Wallia M., Wallia S.M.,

Mitcheed S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Whiting L., Wary P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential).
--- SMILARITY: Belongs to the XK family.
--- CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 414:865-871(2001).
-!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
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                                                                                                                                                                                                                           Huang C.-H., Chen Y.; A superfamily of XK-related genes (XRG) widely expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 579;
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                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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EMBL; AL031658; CAB88102.1; ALT SEQ; Gehomic_DNA.
Ensembl; BNSG0000101321; Homo Fapiens.
HGNC; HGNC:23062; XRR7.
Membrane; Transmembrane.
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Pred. No. 42;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential
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                                                                                                                                                                                                                                                                                                     vertebrates and invertebrates
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                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [MRNA].
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-!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
                                                                                               580
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260
303
323
355
355
415
5415
580 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                          XKR7_RAT
ID XKR7_RAT
AC Q5GH56;
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                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                             Name=XKR7; Synonyms=XRG7;
Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                          Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang C.-H., Chen Y., "A superfamily of XK-related genes (XRG) widely expressed in
                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB 1; Length 579;
Pred. No. 42;
                                                                                                                                                                   Huang C.-H., Chen Y., "A superfamily of XK-related genes (XRG) widely expressed vertebrates and invertebrates.";
                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                              6DFE1191093E85D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
                                                           11-0cT-2005, integrated into UniProtKB/Swiss-Prot. 13-SEP-2005, sequence version 1. 07-FEB-2006, entry version 6. XK-related protein 7.
                                                                                                                                                                                                                                                                                   XX-related protein 7
                                                                                                                                                                                                                                                                                           /FTId=PRO_0000190790
Potential.
                                              579 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              580 AA
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                                                                                                                                                                                                              (Potential).
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Potential.
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Potential.
Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2005, sequence version 1. 07-FBB-2006, entry version 10. Nar.related protein 7. Name=Kkr7; Synonyme=Krg7; Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                63593 MW;
                                                                                                                                                                                                                                                                                                                                                                               51.0%;
                                                                                                                                                                                                                                                                                                                                                                                         58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                            NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 58.3
Matches 7; Conservative
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190 LGQVWRYLRALY 201
   190 LGQVWRYLRALY 201
                                                                                                                                                                                                                                                                                                                                                                                                                   6 LGSIWRFIRAFY 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                              STANDARD;
                                                                                                                                                                                                                                                                           Membrane; Transmembrane
                                                                                                                                                                                                                                                                                                   79
109
280
                                                                                                                                                                                                                                                                                                                                                       415 '
                                                                                                                                          NCBI_TaxID=9598;
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                                                    049LS1;
                             RESULT 10
XKR7_PANTR
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                                              XKR7
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi;
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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"A superfamily of XK-related genes (XRG) widely expressed in "A superfamily of XK-related genes "vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-: SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 50; DB 1; Length 580;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    F3291FABF4C5A826 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-0CT-2005, integrated into UniProtKB/Swiss-Prot. 01-MAR-2005, sequence version 1. 07-FEB-2006, entry version 8. XX-related protein 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XK-related protein 7.
/FTIG=PRO_0000190791.
                                                                                                                                                                                                                       XK-related protein 7./FTId=PRO_0000190789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      580 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                             EMBL; AY534253; AAT07102.1; -; mRNA.
Ensembl; ENSMUSG00000042631; Mus musculus.
MGI; MGI:3526711; Xkr7.
Membrane; Transmembrane.
(Potential).
-!- SIMILARITY: Belongs to the XK family.
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-!- SIMILARITY: Belongs to the XK family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    64302 MW;
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58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [MRNA].
STRAIN=Sprague-Dawley;
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Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 LGQVWRYLRALY 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LGSIWRFIRAFY 17
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07-FEB-2006, entry version 4.
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                                                                                                                                                                                                                     STRAIN=PD1222;
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Q84ZW1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=KAO1;
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Q84ZW1_PEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Larimer F., Land M.; "Annotation of the draft genome assembly of Burkholderia vietnamiensis
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                   US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Burkholderia vietnamiensis G4.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina Copeland A., Lucas S., Lapidus A., Richardson P.; Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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0
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                                                                                                                                                                                                                               Burkholderia vietnamiensis G4.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
            DB 1; Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%; Score 49; DB 2; Length 409; 41.2%; Pred. No. 42;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AAEH02000029; EAM28562.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 409 Aa; 45629 MW; CCD3FA52A9F014E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
Q3PK79 PARDE
ID Q3PK79-PARDE PRELIMINARY; PRT; 449 AA.
AC Q3PK79;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
T 25-OCT-2005, sequence version 1.
                                                                                                                                                                    13-SEP-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                               409 AA.
           Score 50; DB 3
Pred. No. 42;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-G4;
US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US DOE Joint Genome Institute (JGI-PGF);
                                                                                                                                              PRT;
                                                                                                                                                                                 13-SEP-2005, sequence version 1. 07-FEB-2006, entry version 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 GVREMLGHVWQWTRSSY 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GIRRFLGSIWRFIRAFY 17
           58.3%;
                                                                                                                                                                                                                     ORFNames=Bcep1808DRAFT 3388;
                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 41.2'
Matches 7, Conservative
          Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                        || :||::|| |
190 LGQVWRYLRALY 201
                                                           6 LGSIWRFIRAFY 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary data.
                                                                                                                                                                                                       Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                     NCBI_TaxID=269482;
                                                                                                                                            Q4BFM2_BURVI
Q4BFM2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=G4;
                                                                                                                                                                                                                                                                                                        STRAIN=G4;
                                                                                                                     RESULT 13
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Vicieae, Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Paracoccus denitrificans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P., "Sequencing of the draft genome and assembly of Paracoccus denitrificans PD1222.";
                                                                                                     Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteracae; Paracoccus.
NCBL_TaxID=318586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 449;
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Heme; Iron; Metal-binding; Monooxygenase; Öxidoreductase.
SEQUENCE 449 AA; 50659 MW; 5F3EEC9E12AA3B35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PD1222.";
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AAIT01000001; EAN68115.1; -; Genomic_DNA.
GO; GO:0020037; F:heme binding; IEA.
GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:000418; P:electron transport; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR00128; Cytcchrome_P450.
InterPro; IPR00128; Cytcchrome_P450.
PRINTS; PR00463; EP4501.
PRINTS; PR00463; EP4501.
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(64.3%; Pred. No. ac.,
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                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=PD1222;
US DOE Joint Genome Institute (JGI-PGF);
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Cytochrome P450.
ORFNames=PdenDRAFT 4722;
Paracoccus denitrificans PD1222
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9 ROGRGSVWRFIRDF 22
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NUCLEOTIDE SEQUENCE.
TISSUE=Shoot;
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MEDLINE=22417727; PubMed=12529541; DOI=10.1104/pp.012963; Davidson S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.; "The pea gene NA encodes ent-kaurenoic acid oxidase."; Plant Physiol. 131:335-344(2003).
-!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum (By similarity).
-!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                      EMBL; AF537321; AA023063.1; -; mRNA.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:002506; F:heme binding; IEA.

R GO; GO:0005506; F:heme binding; IEA.

R GO; GO:0006497; F:metal ion binding; IEA.

R GO; GO:0006118; P:electron transport; IEA.

R GO; GO:0006118; P:electron transport; IEA.

R InterPro; IPR001128; Cytochrome_P450.

R InterPro; IPR002401; EP4501.

R PANTHER; PTHR19381; Cytochrome_P450; 1.

R PRINTS; RR00465; EP450.

R PRINTS; RR00365; CYTOCHROME_P450; 1.

R PRINTS; PR00365; CYTOCHROME_P450; 1.

R PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%; Score 49; DB 2; Length 488; 58.3%; Pred. No. 50; tive 4; Mismatches 1; Indels
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Matches 7; Conservative
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Search completed: May 19, 2006, 14:38:12 Job time : 115.429 secs

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ZIP: 10036-2811
COMPUTER READABLE FORM:
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Sequence 5105, Ap
Sequence 8162, Ap
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63.384 Million cell updates/sec
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/EMC_Celerra_SIDS3/ptodata/2/jaa/6_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/jaa/H_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/jaa/H_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/jaa/H_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/jaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/jaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/jaa/RE_COMB.pep:*
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-08-940-093-242
US-08-940-096-242
US-09-455-719-242
US-09-455-81-242
US-09-455-81-242
US-09-453-818-242
US-09-453-81-242
US-09-813-81-242
US-09-86-1060-49
US-09-86-1060-45
US-09-88-1060-45
US-09-88-1060-45
US-08-338-882-41
US-09-134-011-279-340
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US-09-134-011-279-340
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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27 44 44.9 22 1 US-08-132-767-50 Sequence 50, Appl 29 44 44.9 589 1 US-08-756-317-5 Sequence 5. Appli 29 44 44.9 1052 2 US-09-134-000C-6620 Sequence 6.20, Appli 31 43.9 413 3 US-10-360-1146-29 Sequence 6.20, Appli 32 US-10-360-1146-29 Sequence 27, Appli 33 43.9 433 3 US-09-609-146-29 Sequence 27, Appli 33 43.9 433 3 US-09-609-146-29 Sequence 29, Appli 34 43 43.9 683 2 US-09-609-146-29 Sequence 25, Appli 35 42 42.9 14 1 US-08-480-190-3 Sequence 15932, Appli 36 42 42.9 14 1 US-08-480-190-3 Sequence 3, Appli 39 42 42.9 14 2 US-09-538 092-643 Sequence 3, Appli 40 42 42.9 14 2 US-08-480-190-3 Sequence 3, Appli 41 42 42.9 15 1 US-08-480-190-2 Sequence 2, Appli 41 42 42.9 15 1 US-08-480-190-2 Sequence 2, Appli 41 42 42.9 15 1 US-08-480-190-2 Sequence 2, Appli 44 42 42.9 15 1 US-08-480-190-2 Sequence 2, Appli 44 42 42.9 15 1 US-08-480-190-2 Sequence 2, Appli 44 42 42.9 15 1 US-08-480-190-2 Sequence 2, Appli 42 42.9 15 1 US-08-480-190-2 Sequence 2, Appli 42 42.9 15 1 US-08-480-190-2 Sequence 2, Appli 44 42 42.9 15 1 US-08-480-190-2 Sequence 2, Appli 45 PCT-US93-07545-2 Sequence 2, Appli 14 PCT-US93-07545-2 Sequence 2, Appli 1
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## ALIGNMENTS

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US-08-940-055-342

US-08-940-055-342

Sequence 242 Application US/08940095

FAPERICANT: Goods and the second and the sequence 242 Application US/08940095

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TYPE: amino a STRANDEDNESS:
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Query Match 79.6%; Score 78; DB 2; Length 18; Best Local Similarity 72.2%; Pred. No. 1.1e-05; Matches 13; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.6%; Score 78; DB 2; Length 18; 72.2%; Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                        CITII NEW CITII NEW CITII NEW COUNTRY: USA
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTRATION UNDER: US/08/940,093
APPLICATION NUMBER: US/08/940,093
FILING DATE: SEE-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/940,093
FILING DATE: APPLICATION NUMBER: OPERATION NUMBER: ATORNEY/AGENT INFORMATION:
NAME: COCULZI, LAURA REGESTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
TELEPHONE: 650-493-556
TELEPHONE: 660-493-556
TELEPRACE GHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                          1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) MOLECULE TYPE: No. 6037323e
US-08-940-093-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 72.23
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                               US-08-940-093-242
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RESULT 3
US-08-940-096-242
Sequence 242, Application US/08940096
Patent No. 6046166
Seneral INFORMATION:

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APPLICANT: Sekul, ...
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
ITILE OF INVENTION: APOLIPOROTEIN A-I ACONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
INUMBER OF SEQUENCES: 258
CORRESPONDENCES: 258
ADDRESSEE: Pennie & Edmonds Lip
STREET: 1155 Avenue of the Americas
CITY: New York

NV
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.6%; Score 78; DB 2; Length 18; 72.2%; Pred. No. 1.1e-05;
                                                                                                                                                                                                                                            CITY: New York
STATE: NY
COMPRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDUIN TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: STEM: DOS
SOFTWARE: Fast SQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: SID
RIGHTON APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUXA A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 009196-0005-999
TELEPHONE: G50-4935
TELEPHONE: G50-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-09-465-719-242
; Sequence 242, Application US/09465719
; Patent No. 6265377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GIKKFLGSIWKFIKAFVG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: No. 6046166e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
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MOLECULE TYPE: No. 6329341e
SEQUENCE DESCRIPTION: SEQ ID NO: 242:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FRALEGO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,838
FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/940,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INPORMATION:
NAME: COCUZZI, LAULA A
REGISTRATION NUMBER: 30,742
REPRENCE/POCKET NUMBER: 0091:
TELECOMMULCATION INPORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GIKKFLGSIWKFIKAFVG 18
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6376464e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA ZIP: 10036-2811 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                               US-09-453-605-242
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US-09-453-838-242
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Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APDILIPOPROTEIN A-1 AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.6%; Score 78; DB 2; Length 18; 72.2%; Pred. No. 1.1e-05;
                                                                                                                                                    FILING DATE:
CLASSIFICATION DATA:
PRIOR PAPELICATION DATA:
PRIOR PAPELICATION DATA:
PRIOR PAPELICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4936
TELEFAX: 66149 FENNIE
INFORMATION FOR SEC ID NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURREY APPLICATION DATA:
APPLICATION NUMBER: US/09/453,605
FILING DATE: 26-NO: 6129341-1999
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION: «UNKNOWN»
PRIOR APPLICATION NUMBER: 08/940,095
FILING DATE: «UNKNOWN»
ATTORNEY/AGBNT INFORMATION:
NAME: COTUZZI, LAUTR A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 242, Application US/09453605
Patent No. 6329341
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: No. 6265377e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 72.23
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
         COMPUTER READABLE FORM:
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US-09-453-605-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-465-719-242
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Sequence 242, Application US/09453838
Sequence 242, Application US/09453838
Patent No. 6376464
GENERAL INFORMATION:
APPLICANT: Bekul, Renate
APPLICANT: Bekul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Gunther, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Difourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
Query Match 79.6%; Score 78; DB 2; Length 18; Best Local Similarity 72.2%; Pred. No. 1.1e-05; Matches 13; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            009196-0004-999
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TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 18 amino acids
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                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dasseux, Jean-Louis
APPLICANT: Bekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: GDEDLY APPLICANT AL AGONISTS AND THEIR
TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                 79.6%; Score 78; DB 2; Length 18; 72.2%; Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30,742
FR: 009196-0007-999
                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,136
FILING DATE: 29-SEP-1997
CLASSIFICATION INFORMATION:
APPLICATION NUMBER: 30,742
APPLICATION NUMBER: 30,742
APPLICATION NUMBER: 30,742
APPLICATION NUMBER: 009196-000
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECHONE: 650-493-4935
TELECHONE: 650-493-4935
TELECHONE: 660-493-556
TELECHONE: 660-493-556
TELECHONE: 660-493-556
TELECHONE: MAIN OF SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: ADDATES
TOTAL OF THE STATEMENT OF THE STATEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 242, Application US/08940136
Patent No. 6518412
GENERAL INFORMATION:
                                                                                                                                                                                                                                         1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                               1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                    Query Match
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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US-09-453-841-242
                                      US-09-453-838-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Suttner, Klaus
APPLICANT: Ocnut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Motor Jean
APPLICANT: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 1.1e-05;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         009196-0004-999
                                                                                                                                                                                                                                                                                                                                 STREET: 1155 Avenue of the Americas CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thing Date:
Classification:
Classification:
PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GIKKFLGSIWKFIKAFVG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: No. 6573239e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 79.6%;
Best Local Similarity 72.2%;
Matches 13; Conservative
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Gentut, Isabelle
APPLICANT: Grout, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: APOLIPOPRESS:
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.6%; Score 78; DB 2; Length 18; 72.2%; Pred. No. 1.1e-05;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELEPOCOMUNICATION INFORMATION:
TELEPAX: 650-491-5556
TELEPAX: 66141 PENNIE
TELERAX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10036-2811
COMPUTER READBALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FREUSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,840
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
FILING DATE:
NAME: COFUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-556
TELEFAK: 660-493-556
INFORMATION FOR SEQ ID NO: 242:
LENGTH: 18 amino acids
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
FOOLOGY: linear
MOLECTLE TYPE: No. 6630450e
US-09-453-826-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-453-840-242
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| Sequence 242, Application US/09453826
| Patent No. 6630450
| GENERAL INFORMATION:
| APPLICANT: Dasseux, Jean-Louis
| APPLICANT: Sekul, Renate
| APPLICANT: Cornut, Isabelle
| APPLICANT: Cornut, Isabelle
| APPLICANT: Ornut, Isabelle
| APPLICANT: Dufourcq, Jean
| APPLICANT: Dufourcq, Jean
| APPLICANT: Dufourcq, Jean
| APPLICANT: APLIPOPROTEIN A-I AGONISTS
| TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
| TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
| NUMBER OF SEQUENCES: 258
| ADDRESSEE: Pennie & Edmonds Lip
| STREET: 1155 Avenue of the Americas
| CITY: New York
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                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-556
TELEPAX: 6614 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IRM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/09/453,826
FILING DATE:
CLASSIPICATION:
                                                                                    ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,833
FILING DATE:
               STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GIXKFLGSIWKFIKAFVG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: No. 6602854e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-453-826-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-453-833-242
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Gaps

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LENGTH: 18 amino acids
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-453-834-242
                                              US-09-453-834-242
                                                                                                                                                                                                                                                                                                                                                                          STATE: NO COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                    Query Match 79.6%; Score 78; DB 2; Length 18; Best Local Similarity 72.2%; Pred. No. 1.1e-05; Matches 13; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.6%; Score 78; DB 2; Length 18; 72.2%; Pred. No. 1.1e-05; Live 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
COMPUTER: IBM COMPALIBLE
COMPARE: ESTSEEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
CLASSIFICATION ATA:
APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6734169e
SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-865-989-242
                                                                                                                                                                                                                                                                                                     RESULT 14
US-09-865-989-242
Squence 242, Application US/09865989
Patent No. 6/34169
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
Sexul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 650-493-4935
TELEFAX: 650-493-556
TELEX: 6614) PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                           1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                     1 GIRRFLGSIWRFIRAFYG 18
TYPE: amino acid
STRANDEDNESS: single
POPOLOGY: linear
HOLECULE TYPE: No. 6716816e
US-09-453-840-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: NY
COUNTRY: USA
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PRICARE SALE MEMBERS AND MANUEL STATES AND MANUE
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Search completed: May 19, 2006, 14:42:54 Job time : 24.8571 secs
                    17-Dec-1999
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                      FILING DATE: 1'
CLASSIFICATION:
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Sequence 242, Application US/09465718

Patent No. 6900177

GENERAL INFORMATION:

APPLICANT: Desseux, Jean-Louis

APPLICANT: Bekul, Renate

APPLICANT: Beturer, Klaus

APPLICANT: Grout, Isabelle

APPLICANT: Metz, Gutcher

TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

ITITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

CORRESPONDENCE ADDRESS:

ADDRESSES: Pennie & Edmonds LLP

STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
                                                                                                                                     STRAIE: Nat

COUNTRY: USA
ZIP: 10036-2811
COMPUTER : 10036-2811
COMPUTER EADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,599
FILING DATE: 29-OCT-2002
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,136
FILING DATE: 29-SEP-1997
ATTORNEY/ACENT INFORMATION:
NAMB: COTUZZi, Laura A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0007-999
TELECOMMUNICATION INFORMATION:
TELEPAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TVDER: AND ACID NO: 242:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 78; DB 2; I
Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
      NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6844327e
US-10-283-599-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 78; DB 2; I
Pred. No. 1.1e-05;
4; Mismatches 1;
                                                           PRICE STETCATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
APPLICATION NUMBER: US/08/940,096
FILING DATE: TATORNEY.
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAUTA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0005-999
TELEPHONE: 650-493-556
TELEPAX: 650-493-556
TELEPAX: 650-493-556
TELEPAX: 66141 PENNIE
APPLICATION NUMBER: US/09/465,718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GIKKFLGSIWKFIKAFVG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
synthyDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6900177e
US-09-465-718-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative
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Sequence:

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Searched:

Database

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1120, App
19, Appl
58, Appl
77, Appl
77, Appl
80, Appl
94, Appl
10, Appl
41, Appl
41, Appl
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US-10-712-447-5
US-10-712-447-5
Sequence 5, Application US/10712447
Publication No. US20040186057A1
GENERAL INFORMATION:
APPLICANT: GARBER, DAVID W.
APPLICANT: DATTA, GEDTA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APPLICANT: DATTA, GEDTA
FILE REFERENCE: 112739-123US
FILE REFERENCE: 112739-123US
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT FILING DATE: 2003-11-13
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
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US-10-712-447-22
US-10-712-447-78
US-10-712-447-120
US-10-712-447-120
US-10-712-447-56
US-10-712-447-58
US-10-712-447-77
US-10-712-447-79
US-10-712-447-94
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US-10-712-447-91
US-10-712-447-41
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; OTHER INFORMATION: c-term amidated
US-10-712-447-2
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ORGANISM: Artificial Seguence
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LENGTH: 18
      Query Match
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Sequence 8, Appli
Sequence 10, Appli
Sequence 11, Appl
Sequence 115, Appl
Sequence 116, Appl
Sequence 117, Appl
Sequence 117, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 11, Appl
Sequence 61, Appl
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/ EMC Celerra SIDS3/prodata/2/pubpaa/US08_PUBCOMB.pep.*
/ EMC Celerra SIDS3/prodata/2/pubpaa/US09_PUBCOMB.pep.*
/ EMC Celerra SIDS3/prodata/2/pubpaa/US108_PUBCOMB.pep.*
/ EMC Celerra SIDS3/prodata/2/pubpaa/US108_PUBCOMB.pep.*
/ EMC Celerra SIDS3/prodata/2/pubpaa/US108_PUBCOMB.pep.*
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102.575 Million cell updates/sec
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                                                                                                               ; Search time 81.2857 Seconds
                     GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-712-447-5
US-10-712-447-10
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US-10-712-447-113
US-10-712-447-115
US-10-712-447-115
US-10-712-447-129
US-10-712-447-129
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US-10-712-447-129
US-10-712-447-129
US-10-712-447-129
US-10-712-447-119
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                May 19, 2006, 15:18:19
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Maximum DB seq length: 2000000000
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Perfect score:
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Sequence 8, Application US/10712447

Publication No. US2040186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: APOLIPPROPROTEIN E AND METHODS OF USE

FILE REBERENCE: 112739-1230S

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT PILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

PRIOR FILING DATE: 2002-11-13

SOFTWARE: Patentin Ver. 3.2

SEQ ID NO 8

LENGTH: 18
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US-10-712-447-10

Sequence 10, Application US/10712447

Sequence 10, Application US/10712447

Sequence 10, Spiloston US/10712447

Sequence 10, US20040186057A1

GENERAL INFORMATION:
APPLICANT: ARABER DAVID W.
APPLICANT: ARABER DAVID W.
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210
                                                                                                                                     ; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-712-447-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: 60/425,821
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 5
LENGTH: 18
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APPLICANT: GARBER, DAVID W.
APPLICANT: DATTA, GEETA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILE REFERENCE: 112739-123US
CURRENT APPLICATION NUMBER: US/10/712,447
PRIOR PELLING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: 60/425,821
PRIOR PELLING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PATENTIN Ver. 3.2
LENGTH: 18
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US-10-712-47-91
IS Equence 91, Application US/10712447
Publication No. US20040186057A1
GENERAL INFORMATION:
APPLICANT: GARBER, DAVID W.
APPLICANT: DATTA, GEETA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIDOPROTEIN E AND METHODS OF USE
TILE OF INVENTION: APOLIDOPROTEIN E AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT FILIG DATE: 2003-11-13
                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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Best Local Similarity 100.0%; Pred. No. 9.8e-08; Matches 18; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO SEQ ID NOS: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-10-712-447-13
Sele-normal Application US/10712447
Publication No. US20040186057A1
GENERAL INFORMATION:
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                                                                                                ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 3.2 SEQ ID NO 10 LENGTH: 18 TYPE: PRT
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Matches 18; Conservative
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RESULT 9
US-10-712-447-117
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; Sequence 116, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: ANANTHON WANTHER, DOWNIN POLYPEPTIDES MIMICKING; TITLE OF INVENTION: SYNTHETIC SINGLE DOWNIN POLYPEPTIDES MIMICKING; TITLE OF INVENTION: APPLICATION NUMBER: US/10/712,447
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT PLING DATE: 2003-11-13
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 116
; TENGRAL INFORMATION NUMBER: AND SEQ ID NO 116
; TENGRAL INFORMATION NUMBER: AND SEQ ID NO 116
; TENGRAL INFORMATION NUMBER: AND SEQ ID NO 116
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; TENGRAL INFORMATION NUMBER: AND SEQ ID NO 116
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| Sequence 115, Application US/10712447 |
| Sequence 115, Application US/10712447 |
| Publication No. US20040186057A1 |
| GENERAL INFORMATION |
| APPLICANT: ANANTHARAMIAH, GATTADAHALLI M. |
| APPLICANT: GARBER, DAVID W. |
| APPLICANT: GARBER, US/10 W. |
| APPLICANT: DATTA, GEETA |
| TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING |
| TITLE OF INVENTION: APPLICATION NUMBER: US/10/712,447 |
| CURRENT APPLICATION NUMBER: US/10/712,447 |
| PRIOR APPLICATION NUMBER: 60/425,821 |
| PRIOR PILING DATE: 2002-11-13 |
| NUMBER OF SEQ ID NOS: 210 |
| SEQ ID NO 115 |
| LENGTH: 18
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                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Synthetic JOTHER INFORMATION: peptide US-10-712-447-91
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                                                                                                                                                                                                                                Query Match 96.9%; Score 95; DB 4; Length 18; Best Local Similarity 94.4%; Pred. No. 2.8e-07; Matches 17; Conservative 1; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
FEATURE:
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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Sequence 117, Application US/10712447

Sequence 117, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANATHRARMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION NUMBER: US/10/712,447

CURRENT APPLICATION NUMBER: US/10/712,447

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PALENTIN Ver. 3.2

LENGTH: 18
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APPLICANT: GARBER, DAVID W.
APPLICANT: GARBER, DAVID W.
APPLICANT: DATTA, GETTA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
TILE REFERENCE: 112739-123US
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT FILING DATE: 2003-11-13
PRIOR PILING DATE: 2003-11-13
PRIOR PILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PATENTIN VOY: 3.2
SEQ ID NO 129
LENGTH: 18
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
JOHER INFORMATION: peptide
US-10-712-447-129
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide
US-10-712-447-116
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                                                                                                                        Length 18
                                                                                                                                                                         2; Mismatches
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Publication No. US20040186057A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                        Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
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ORGANISM: Artificial Sequence
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Mismatches
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                                                                                                    1 GIRRFLGAIWRFIRSFYG 18
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Best Local Similarity 88.9%;
Matches 16; Conservative
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ORGANISM: Artificial Sequence
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LOCATION: (14)
OTHER INFORMATION: (DiMe)Lys
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16, Conservative
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NAME/KEY: MOD_RES
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                                                                                                                                                                                                                                                                                              Sequence 131, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: ANANTHON: SYNTHEITC SINGLE DOMAIN POLYPEPTIDES MIMICKING

ITILE OF INVENTION: SYNTHEITC SINGLE DOMAIN POLYPEPTIDES MIMICKING

ITILE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

FILE REFERENCE: 112739-123US

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT PILING DATE: 2003-11-13

PRIOR PILING DATE: 2002-11-13

PRIOR PILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENTIN VET: 3.2

LENGTH: BR
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APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: GARBER, DAVID W.
APPLICANT: DATTA, GBETA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILE REFERENCE: 112739-123US
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT FILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PATENTING OF SEQ ID NOS: 210
SOFTWARE: PATENTING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PATENTING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PATENTING DATE: 2004-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
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US-10-712-447-131
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US-10-712-447-21
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                        Score 94; DB 4; Length 18;
Pred. No. 3.9e-07;
2; Mismatches 0; Indels
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Pred. No. 7.9e-07;
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Publication No. US20040186057A1
GENERAL INFORMATION:
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88.9%;
                           Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity
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RESULT 14
US-10-712-447-74
is Sequence 74, Application US/10712447
sequence 74, Application US/10712447
spublication No. US20040186057A1
is GENERAL INFORMATION:
is APPLICANT: ANTHARAMIAH, GATTADAHALLI M.
is APPLICANT: GARBER, DAVID W.
is APPLICANT: DATTA, GEETA
if TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
if TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
if TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
if CURRENT APPLICATION NUMBER: US/10/712,447
if CURRENT FILING DATE: 2003-11-13
if PRIOR FILING DATE: 2002-11-13
if NUMBER OF SEQ ID NOS: 210
if SOFTWARE: PATENTIN Ver. 3.2
if SEQ ID NO 74
if LENGTH: 18
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Sequence 53, Application US/10712447

Publication No. US2004018605741

Sequence 53, Application US/10712447

Publication No. US2004018605741

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: GARBER, DAVID W.

APPLICANT: GARTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLICADOR OF USE

TITLE OF INVENTION: APOLICATION NUMBER: US/10/712,447

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PALENTIN Ver. 3.2

LENGTH: 18
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Gaps
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Indels
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US-10-712-447-4

; Sequence 4, Application US/10712447

; Publication No. US20040186057A1

; APPLICANT: ANATHARAMIAH, GATTADAHALLI M.

; APPLICANT: DATTA, GEETA

; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

; TURRENT APPLICATION NUMBER: US/10/712,447

; CURRENT FILING DATE: 2003-11-13

; PRIOR PILING DATE: 2003-11-13

; PRIOR PILING DATE: 2003-11-13

; PRIOR FILING DATE: 2003-11-13

; SEQ ID NO 4

; LENGTH: 18

TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide

US-10-712-447-4
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Best Local Similarity 94.4%; Pred. No. 1.6e-06;
Matches 17; Conservative 0; Mismatches 1; Indels
                                                                             Query Match 93.9%; Score 92; DB 4; Length 18; Best Local Similarity 88.9%; Pred. No. 7.9e-07; Matches 16; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                           1 GIRKFLGSIWRFIKAFYG 18
                                                                                                                                                                                           1 GIRRFLGSIWRFIRAFYG 18
; OTHER INFORMATION: peptide US-10-712-447-74
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Search completed: May 19, 2006, 15:27:56 Job time: 81.2857 secs

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US-11-242-505A-18
Sequence 18, Application US/11242505A
Publication No. US20060099656A1
GENERAL INFORMATION:
APPLICANT: Carroll, Joseph M.
APPLICANT: Healy, Alleen
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Query Match
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Matches
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Sequence 18, Appl
Sequence 112, Appl
Sequence 111, Appl
Sequence 5, Appli
Sequence 2540, Appli
Sequence 2540, Appli
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109, App
7, Appli
40, Appl
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/ RMC Celerra SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.ppp:*/
/ RMC Celerra SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.ppp:*/
/ RMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.ppp:*/
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/ RMC Celerra SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.ppp:*/
/ RMC Celerra SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.ppp:*/
/ RMC Celerra SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.ppp:*/
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           GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-949-925-142

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US-11-242-505A-48

US-11-242-505A-48

US-10-511-937-2540

US-10-975-692-2

US-11-169-140-109

US-11-204-427-7

US-11-304-427-7

US-11-304-429-48

US-11-304-429-40

US-11-308-853

US-10-505-928-853

US-10-505-928-853

US-10-505-928-853

US-10-130-918-853

US-10-105-928-9545

US-10-105-928-9545

US-10-105-928-9545

US-10-105-928-9545

US-10-105-928-9545

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US-10-105-928-9336

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US-11-251-465-18
US-11-261-384-2
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                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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APPLICANT: Wohlgemuch, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Prentice, James
APPLICANT: Marchonald
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
TITLE OF INVENTION: AND MONITORING TRANSPLANT
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: Patentin version 3.2
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US-11-223-738-6
US-11-312-958-48
US-11-024-5448-21
US-11-190-750-135
US-11-264-784-87
US-10-504-123
US-10-504-123
US-10-505-920-163
US-10-505-920-163
US-10-505-920-163
US-10-504-120-19
US-10-504-120-19
US-10-504-120-19
US-11-311-55-16
US-10-505-928-443
US-11-321-654-44
US-11-257-062-44
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; Pred. No. 15;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: EXPRESSION DIAGNOSTICS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2947, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
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1503
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222
222
282
282
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ORGANISM: Homo sapiens
US-10-511-937-2947
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nes 7; Conserv
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34021, 44099, 25278,
62553, 302, 323,
2058 OR 6351 MOLECULES.
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                Length 60;
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APPLICANT: Millenium Pharmaceuticals, Inc.
APPLICANT: Silos-Santiago, Immaculada
APPLICANT: Venkateswarlu, Karicheli
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559,
TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656,
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318,
FILE REPERENCE: MPIO2-012PIRNM_OMNI
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                                                                                            3; Indels
        Score 36.5; DB 1;
Pred. No. 2.2;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al.

APPLICANT: Rosen et al.

TITLE OF INVENTION: 67 Human secreted proteins
FILE REFERENCE: P2023P2
CURRENT APPLICATION NUMBER: US/09/949,925
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 60/232,150
PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: PCT/US99/01621
PRIOR FILING DATE: 1990-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
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PRIOR PILING DATE: 1998-01-30
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OTHER INFORMATION: Xaa equals stop translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 111, Application US/09949925
Publication No. US20060099575A9
GENERAL INFORMATION:
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                37.2%;
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                                                                                                                                                                    5 FLGSIWRFIRAFYG 18
                                                                                                                                                                                                                    31 FLILVWIFV-AFYG 43
                Query Match
Best Local Similarity 57.1
Matches 8; Conservative
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59 LREVSGKIWRF 69
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Matches 6, Conserv
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NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                         JS-09-949-925-111
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US-11-302-678-5
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TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12849, 13875,
TITLE OF INVENTION: 14395, 14641, 1762, 58874, 252, 304, 1980, 14717, 9941, 19310,
FILE REPRENCE: MPI2001-288PIRCPICMAIN
CURRENT FILING DATE: 2002-10-03
CURRENT FILING DATE: 2002-11-07
PRIOR PRILOR APPLICATION NUMBER: US 10/290,078
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2001-11-07
SPRIOR FILING DATE: 2001-11-07
SPRIOR FILING DATE: 2001-12-17
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Fublication No. US2060099575A9
GENERAL INPORMATION:
TITLE OF INVENTION: 67 Human secreted proteins
FILE REFERENCE: PZ021P2
CURRENT APPLICATION NUMBER: US/09/949,925
CURRENT APPLICATION NUMBER: US 60/232,150
FRIOR PRIOR PELLING DATE: 2000-10-0
FRIOR PELLING DATE: 1999-01-2
FRIOR PELLING DATE: 1999-01-27
FRIOR FILLING DATE: 1999-01-30
FRIOR FILLING DATE: 1999-01-30
FRIOR FILLING DATE: 1998-01-30
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US-09-949-925-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 37.8%;
Best Local Similarity 55.6%;
Matches 5; Conservative 3
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155 VRRVLGAVW 163
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ORGANISM: Homo Sapiens
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ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/11/302,678

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## APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION
### APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION
### APPLICANT: Wallis, James G
### TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF
### TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS
### TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS
### TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS
### TITLE OF INVENTION: UNBER: US/10/975,692
### CURRENT FILING DATE: 2004-10-26
### PRIOR FILING DATE: 1999-12-06
### PRIOR FILING DATE: 1999-12-07
### PRIOR FILING DATE: 1999-12-07
### NUMBER OF SEQ ID NOS: 17
### SOFTWARE: PatentIn version 3.3
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APPLICANT: WOLLWALL, NOUTE,
APPLICANT: Prentice, James
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: ROSenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: MAD MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2003-04-19
PRIOR FILING DATE: 2003-04-24
PRIOR FILI
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Pred. No. 44;
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                                                                                                                                                                                                                                  Sequence 2540, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/10975692
Publication No. US20060090221A1
GENERAL INFORMATION:
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; ORGANISM: Caenorhabditis elegans
US-10-975-692-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 46.2%;
Matches 6; Conservative
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Woodward, Robert
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195 LEEAWSFLDAFY 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Homo sapiens
US-10-511-937-2540
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APPLICANT: Healy, Aileen
APPLICANT: Healy, Aileen
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 14717, 9941, 19310,
TITLE OF INVENTION: HASS, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
FILE REFERENCE: MPIZOR1-288PIRCPIOMNIM
CURRENT APPLICATION NUMBER: US 10/290,078
PRIOR FILING DATE: 2005-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR PELICATION NUMBER: US 60/347,949
PRIOR FILING DATE: 2001-12-16
PRIOR FILING DATE: 2001-12-16
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 313
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36.7%; Score 36; DB 7; Length 599;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 0; Indels
                                                              PRIOR APPLICATION NUMBER: US/10/345,680
PRIOR FILING DATE: 2003-01-16
PRIOR FILING DATE: 2003-01-16
PRIOR PELING DATE: 2002-01-19
PRIOR PELING DATE: 2002-01-19
PRIOR PELING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/360,500
PRIOR APPLICATION NUMBER: US 60/365,041
PRIOR APPLICATION NUMBER: US 60/365,041
PRIOR PILING DATE: 2002-03-15
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-06-14
PRIOR PILING DATE: 2002-06-14
PRIOR PILING DATE: 2002-09-27
PRIOR PILING DATE: 2002-09-27
PRIOR PILING DATE: 2002-09-27
PRIOR PILING DATE: 2002-10-21
PRIOR PILING DATE: 2002-10-21
PRIOR PILING DATE: 2002-10-21
PRIOR PILING DATE: 2002-11-05
PRIOR PILING DATE: 2002-11-05
PRIOR PILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FASTERO for Windows Version 4.0
SEG ID NO 5
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US-11-242-505A-48
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64 LGNVWRF 70
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GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: MASUDA, Yasushi

APPLICANT: MASUDA, Yasushi

APPLICANT: WATANBB, Takuya

APPLICANT: TERAO, Yasush

APPLICANT: TERAO, Yasush

APPLICANT: TERAO, Yasush

APPLICANT: TERAO, Yasush

APPLICANT: HINUMA, Saush

APPLICANT: HINUMA, Saush

ITILE OF INVERTION: Novel Physiologically Active Peptide and Use Thereof

FILE REFERENCE: 2762USOP

CURRENT APPLICATION NUMBER: US/11/304,129

FRIOR APPLICATION NUMBER: US/200-12-15

PRIOR APPLICATION NUMBER: US 2000-217442

PRIOR APPLICATION NUMBER: JP 2000-217442

PRIOR APPLICATION NUMBER: JP 2001-26-79

PRIOR APPLICATION NUMBER: PCT/JP01/06162

PRIOR APPLICATION NUMBER: PCT/JP01/06162

PRIOR APPLICATION NUMBER: PCT/JP01/06162

PRIOR PILING DATE: 2001-07-17

NUMBER OF SEQ ID NO 40

- TEMPORTY IN ADDITION NUMBER: DCT/JP01/06162

FRIOR PILING DATE: 2001-07-17

NUMBER OF SEQ ID NO 40
                                                                                              Gaps
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                          Length 244;
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Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.7%; Score 33; DB 7; Length 342; 50.0%; Pred. No. 63;
                                                                                           3; Indels
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                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/11204427

Publication No. US20060100146A1

GENERAL INFORMATION:

APPLICANT: Sturley, Stephen L

APPLICANT: Crouley, Debra

APPLICANT: Crouley, Debra

TITLE OF INVENTION: AMAT-RELATED METHODS AND ARTICLES

FILE REFERENCE: 0575/72796/JPW/AJM/JCS

CURRENT APPLICATION NUMBER: US/11/204,427

CURRENT FILING DATE: 2005-08-15

NUMBER OF SEQ ID NOS: 73

SOFTWARE: PatentIn version 3.3
                                DB 7;
                             Query Match
34.2%; Score 33.5; D
Best Local Similarity 42.1%; Pred. No. 35;
Matches 8; Conservative 3; Mismatches
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Publication No. US20060088915A1
GENERAL INFORMATION:
                                                                                                                                                                                                                       158 GLVLALGAVWCVARARFIR 176
                                                                                                                                                         1 GIRRFLGSIW----RFIR 14
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Best Local Similarity
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US-11-304-129-40
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US-11-304-129-40
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Publication No. US200600991501

Publication No. US200600991501

GENERAL INPORMATION:

APPLICANT: ARIZEKE PHARMACEUTICALS, INC.

APPLICANT: HUGSTON, Lou, L.

APPLICANT: GLYN, Jacqueline, M.

APPLICANT: GLYNN, Jacqueline, M.

APPLICANT: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CF

TITLE OF INVENTION: BARRIERS

FILE REPERENBENCE: 11474-037-999

CURRENT FILING DATE: 2001-02-09

FRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-11-13

PRIOR FILING DATE: 2000-11-09-06

PRIOR FILING DATE: 2001-09-06

PRIOR APPLICATION NUMBER: 09/949,039

PRIOR FILING DATE: 2001-09-06

PRIOR FILING DATE: 2001-10-02

PRIOR FILING DATE: 2001-10-03

PRIOR FILING DATE: 2001-10-02

PRIOR FILING DATE: 2001-10-02

PRIOR FILING DATE: 2001-10-02

PRIOR FILING DATE: 2001-10-03

PRIOR FILING DATE: 2001-10-03
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34.7%; Score 34; DB 6; Length 447;
43.8%; Pred. No. 59;
tive 4; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                  Sequence 543, Application US/10505928

Publication No. US20060088532A1

GENERAL INFORMATION:

APPLICANT: Ludwig Institute for Cancer Research et al.

TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

FILE REFERENCE: 28967/39178

CURRENT APPLICATION NUMBER: US/10/505,928

CURRENT FILING DATE: 2004-08-27

PRIOR FILING DATE: 2004-08-27

NUMBER OF SEQ ID NOS: 866

SOFTWARE: Patentin 3.2

SEQ ID NO 543

LENGTH: 522
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SEQ ID NO 109
LENGTH: 244
TYPE: PRT
                                                                                                                               2 IRRFLGSIWRFIRAFY 17
   Query Match
Best Local Similarity 43.8<sup>†</sup>
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-543
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US-11-169-140-109
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US-10-505-928-543
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Score 33; DB 6; Length 1531;
Pred. No. 3.6e+02;
3; Mismatches 3; Indels
                                                                                                                                                                         APPLICANT: LOUGHING INSTITUTE for Cancer Research et al.
TILE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR PELICATION NUMBER: US 60/363,019
PRIOR PILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE PARENTIN 3.2
LENGTH: 1531
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Job time : 2.14286 secs
                                                                RESULT 15
US-10-505-928-853
Sequence 853, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
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Best Local Similarity 50.0%;
Matches 6; Conservative
339 RYYSSEYHYVGGFYG 353
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1122 LGLIYFFVQRFY 1133
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; ORGANISM: Homo sapiens
US-10-505-928-853
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US-11-304-129-48

Sequence 48, Application US/11304129

Sequence 48, Application No. US20060088915A1

GENERAL INFORMATION:

APPLICANT: OHTAKI, Tetsuya

APPLICANT: MASUNA, Yasushi

APPLICANT: TAKATSU, Yoshihiro

APPLICANT: TERAO, Yasushi

APPLICANT: TERAO, Yasushi

APPLICANT: TERAO, Yasushi

APPLICANT: TERAO, Yasushi

APPLICANT: SHINTANI, Yasushi

FILE REFERENCE: 2762USOP

CURRENT FILING DATE: 2003-09-29

FRIOR FILING DATE: 2003-09-29

FRIOR APPLICATION NUMBER: US/10/33,192

FRIOR FILING DATE: 2001-07-18

FRIOR APPLICATION NUMBER: DET/JP01/06162

FRIOR FILING DATE: 2001-02-02

FRIOR APPLICATION NUMBER: PCT/JP01/06162

FRIOR FILING DATE: 2001-07-17

WUMBER OF SEQ ID NOS: 58

LENGTH: 393
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Publication No. US2006088532A1

GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TILE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178

CURRENT APPLICATION NUMBER: US/10/505,928

CURRENT APPLICATION NUMBER: US 60/363,019

PRIOR PILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 866

SOFTWARE: Patentin 3.2

LENTH: 463
    Indels
    9
  1; Mismatches
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Best Local Similarity 46.2%;
Matches 6; Conservative
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Best Local Similarity 33.3
Matches 5; Conservative
                                               5 FLGSIWRFIRAFY 17
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    6; Conservative
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US-10-505-928-545
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       Matches
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4 RFLGSIWRFIRAFYG 18

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Gaps

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24 86 87.8 18 8 AD034305 Ado34305 Synthetic 26 85 86.7 18 8 AD034305 Ado34344 Synthetic 27 85 86.7 18 8 AD034345 Ado34344 Synthetic 28 86.7 18 8 AD034345 Ado34345 Synthetic 29 84 85.7 18 8 AD034301 Ado34301 Synthetic 30 84 85.7 18 8 AD034301 Ado34301 Synthetic 31 85.7 18 8 AD034302 Ado34301 Synthetic 32 83.7 18 8 AD034302 Ado34302 Synthetic 33 82 83.7 18 8 AD034302 Ado34302 Synthetic 36 83.7 18 8 AD034303 Ado34302 Synthetic 36 83.7 18 8 AD034303 Ado34303 Synthetic 36 83.7 18 8 AD034303 Ado34302 Synthetic 36 83.7 18 8 AD034303 Ado34303 Synthetic 36 83.7 18 8 AD034302 Ado34303 Synthetic 36 83.7 18 8 AD034302 Ado34303 Synthetic 37 82 83.7 18 8 AD034303 Ado34303 Synthetic 37 82 83.7 18 8 AD034303 Ado34303 Synthetic 38 82 83.7 18 8 AD034303 Ado34303 Synthetic 39 81 82.7 18 8 AD034323 Ado34303 Synthetic 37 82 83.7 18 8 AD034323 Ado34303 Synthetic 37 80.6 18 8 AD034323 Ado34320 Synthetic 42 79 80.6 18 8 AD034320 Ado34320 Synthetic 42 78 79.6 18 2 AAY19371 Ad034303 Lecithin: Ad034310 Ad034325 Lecithin:	RESULT 1 AD034231 ID AD034231 ID AD034231 ID AD034231; XZ AD034231; XX AD03422004; XX AD015poprotein-E mimicking polypeptide, SEQ ID No 8. XX AD015poprotein-E mimicking polypeptide, antilipaemic, cardiant, XX AD04202; antiarterioscleroric, carebroprotective, antiarginal, XX AD0404043403-A2. XX AD0404043403-A2. XX AD0404044303-A2. XX AD04040400. XX AD04040400. XX AD04040400. XX AD04040400. XX AD04040400. XX AD04040400. XX AD040401629, 200206-0425821P. XX AD04040401629, 200206-0425821P. XX AD04040401629, 200206-0425821P. XX AD040401629, 20040401629, 20040401629, 200506-0425801P. XX AD040401629, 20040401629, 200506-0425801P. XX AD04040401629, 20040401629, 20040401629, 200506-0425801P. XX AD04040401629, 20040401629, 20040401629, 20040401629, 20040401629, 20040401629, 2004040401629, 2004040401629, 2004040401629, 2004040401629, 2004040401620000000000000000000000000000	Synth Comprocessing the interval of the interv
ion 5.1.8  lo6 Biocceleration Ltd.  le1  Search time 94.2857 Seconds (without alignments) 87.287 Million cell updates/sec seidues  residues  1589679	chance to haw result being 1 stribution. bescript.  Descript.  Ad034231 Ad034238 Ad034314 Ad034314 Ad034314 Ad034314	Ado34238 Synthetic Ado34340 Synthetic Ado34230 Synthetic Ado34230 Synthetic Ado34227 Synthetic Ado3427 Synthetic Ado3427 Synthetic Ado34350 Synthetic Ado34350 Synthetic Ado34318 Synthetic Ado3433 Synthetic Ado3431 Synthetic Ado3431 Synthetic Ado3431 Synthetic Ado3424 Synthetic Ado3424 Synthetic Ado3424 Synthetic
GenCore vere GenCore vere search, using sw moc 19, 2006, 14:13:22 ; 0-712-447-8 RRFLGSIWRFIRAFYG 18 UM62 p 10.0 , Gapext 0.5 679 seqs, 457216429 ; satisfying chosen pe	hh: 0  timum Match 10  geneseqp200018  geneseqp20003  geneseqp20003  geneseqp20003  geneseqp20003  geneseqp20003  geneseqp20003  than or equal	95.9 18 8 AD034338 95.9 18 8 AD034339 95.9 18 8 AD034339 93.9 18 8 AD034297 93.9 18 8 AD034297 91.8 18 8 AD034227 91.8 18 8 AD034227 91.8 18 8 AD034322 89.8 18 8 AD034335 89.8 18 8 AD034335 89.8 18 8 AD034337 89.8 18 8 AD034337 89.8 18 8 AD034241 89.8 18 8 AD034241 89.8 18 8 AD034241
Coy  OM protein - protein  Run on:  Title: Perfect score: 98 Sequence: 1 GII Scoring table: BLOS Searched: 2589 Total number of hits	Pred No Score green and is der green and is der green	10 9 9 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, caradiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antiarginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of mycardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
                                                                                                                                                                                                                                                                                                                                                                                                                        mimicking polypeptide of the invention.
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Sequence 18 AA;

Gaps ; 0 100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 6.4e-08; 0; Indels 0; Mismatches 1 GIRRFLGSIWRFIRAFYG 18 18; Conservative Best Local Similarity Query Match Matches ò

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RESULT 2 ADO34225

ADO34225 standard; peptide; 18 AA. ADO34225;

12-AUG-2004 (first entry)

Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholestreol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL. 

Synthetic.

note= "N-terminal acetyl" /note= "C-terminal amide" Location/Qualifiers Key Modified-site Modified-site

WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

UABR-) UAB RES FOUND

Datta G; Anantharamiah GM, Garber DW, WPI; 2004-411629/38 Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 2; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

minicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E minicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E minicking polypeptide and a carrier; and an amonoclonal antibody that specifically binds to the synthetic apolipoprotein-E minicking polypeptide has the following activities; antilippemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E minicking polypeptide has the following activities; antilippemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E minicking polypeptide is cusful for reducing serum cholesterol in a subject (including a mammal cuscul as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for treating coronary artery disease, composardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E minicking polypeptide enhances bluding of low-density lipoprotein of LDL or cyllob by a cell. This sequence represents a synthetic apolipoprotein-E comminicking polypeptide of the invention. ö Gaps apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDL; cell, a recombinant cell or a transgenic, non-human subject ; Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 5. Length 18; 0; Indels 100.0%; Score 98; DB 8; 100.0%; Pred. No. 6.4e-08; Mismatches Ś ö ADO34228 standard; peptide; 18 1 GIRRFLGSIWRFIRAFYG 18 1 GIRRFLGSIWRFIRAFYG 18 13-NOV-2003; 2003WO-US036268. 13-NOV-2002; 2002US-0425821P Query Match
Best Local Similarity 100...
Best Local 18; Conservative 12-AUG-2004 (first entry) (UABR-) UAB RES FOUND. WO2004043403-A2 Sequence 18 AA; 27-MAY-2004. Synthetic ADO34228; RESULT 3 AD034228 ò g 

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. Datta G; Claim 4; SEQ ID NO 5; 79pp; English Garber DW, WPI; 2004-411629/38. Anantharamiah GM,

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minicking polypeptide encoding polypuclectide; a composition comprising
the synthetic apolipoprotein-E minicking polypeptide and a carrier; and
an monoclonal antibody that specifically binds to the synthetic
an monoclonal antibody that specifically binds to the synthetic
an monoclonal antibody that specifically binds to the synthetic
cardiant, wasotropic, antiarteriosclerotic, cerebroprotective, and
cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
antianginal. The synthetic apolipoprotein-E minicking polypeptide is
useful for reducing serum cholesterol in a subject (including a mammal
such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
chimpanzee or orangutan); for treating coronary artery disease,
chimpanzee or treating angina. The synthetic apolipoprotein the subject;
and also for treating angina. The synthetic apolipoprotein E minicking
polypeptide enhances binding of low-density lipoprotein (LDL) or very low
density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
which in a synthetic apolipoprotein-E
or plant) comprising the synthetic apolipoprotein-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mimicking polypeptide of the invention
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Sequence 18 AA;

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Gaps
                          ;
100.0%; Score 98; DB 8; Length 18;
                        0; Indels
              6.4e-08;
                          0; Mismatches
              Pred. No.
                                                   1 GIRRFLGSIWRFIRAFYG 18
               100.0%;
                          18; Conservative
             Best Local Similarity
Matches 18; Conserv
  Query Match
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셤 ADO34236 standard; peptide; 18 AA. AD034236; 

12-AUG-2004 (first entry)

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; oconnary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDL; Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 13.

Synthetic

402004043403-A2.

27-MAY-2004

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P.

(UABR-) UAB RES FOUND.

Anantharamiah GM, Garber DW, Datta WPI; 2004-411629/38. Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 13; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising

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cc the synthetic apolypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monocolonal antibody that specifically binds to the synthetic and an expecifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and cusful for reducing serum cholesterol in a subject (including a mammal cusful for reducing serum cholesterol in a subject (including a mammal cusful for reducing serum cholesterol in a subject (including a mammal confinement or artherosclerosis, and correction or stroke, for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking collypeptide enhances binding of low-density lipoprotein (VLDE) to a cell and enhances degradation of LDE or VLDE by a cell. This sequence represents a synthetic apolipoprotein-E communicking polypeptide che invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina: low-density lipoprotein; LDL; very low density lipoprotein; LDL.
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                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 6.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Conservative
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                                                                                                                                                                                                                                                                                                                                                         Sequence 18 AA;
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the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiatreriosoclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal cuch as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for breaking and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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Sequence 18 AA;

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Length 18;
                                0; Indels
100.0%; Score 98; DB 8; I
100.0%; Pred. No. 6.4e-08;
iive 0; Mismatches 0;
                                                                1 GIRRFLGSIWRFIRAFYG 18
                                                                                              1 GIRRFLGSIWRFIRAFYG 18
                Local Similarity 100.
les 18; Conservative
    Query Match
                   Best Loca
Matches
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Gaps ; 0

> RESULT 6 AD034314

ADO34314 standard; peptide; 18 AD034314; 

(first entry)

12-AUG-2004

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Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 91.

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction, stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

Synthetic

WO2004043403-A2.

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

Anantharamiah GM, Garber DW,

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. WPI; 2004-411629/38.

Datta G;

Claim 4; SEQ ID NO 91; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypeotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic

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cc an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E minicking polypeptide. The synthetic apolipoprotein-E cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and cantianginal. The synthetic apolipoprotein-E minicking polypeptide is antianginal. The synthetic apolipoprotein-E minicking polypeptide is cuseful for reducing serum cholesterol in a subject (including a mammal csuch as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, composatelipoproteinamia or atherosclerosis; and for reducing the risk of composatelipoprotein and also for treating angina. The synthetic apolipoprotein. E minicking polypeptide enhances binding of low-density lipoprotein (UDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein. E minicking polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
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                                                                                                                                                                                                                                                                                            Score 95; DB 8; Length Lu,
Pred. No. 1.8e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                  1 GIRKFLGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                               96.98;
                                                                                                                                                                                                                                                                                                                              94.48;
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                                                                                                                                                                                                                                                                                Sequence 18
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Matches
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us-10-712-447-8.rag

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apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipeemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is cardiant for reducing serum cholesterol in a subject (including a mammal cueful for reducing serum cholesterol in a subject (including a mammal cueful for reducing serum cholesterol in a subject (including a mammal chimpensee or orangutuan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or attrove; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking colypeptide enhances binding of low-density lipoprotein (ULDL) to a cell and enhances (degradation of LDL) or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 115.
                                                                                                                                                                                                                                                                               Length 18;
                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                              95.9%; Score 94; DB 8; I
88.9%; Pred. No. 2.6e-07;
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                                                                                                                                                                                                                                                Sequence 18 AA;
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Gape

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0; Indels

2; Mismatches

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1 GIRRFLGSIWRFIRAFYG 18

16; Conservative

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ADO34352 standard; peptide; 18

RESULT 9 AD034352

Score 94; DB 8; Length 18; Pred. No. 2.6e-07;

95.9%;

Query Match Best Local Similarity

Sequence 18 AA;

cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinadmia or atherosclerosis; and for reducing the risk of myocardial infarction or atherosclerosis; and for reducing the subject, and also for treating angina. The synthetic apolipoprotein (in subject) polypeptide enhances binding of low-density lipoprotein (in [DL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein. E mimicking mimicking polypeptide of the invention.

mimicking polypeptide has the following activities: antilipaemic,

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polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and apolipoprotein-E mimicking polypeptide and a carrier; and apolipoprotein-E mimicking polypeptide apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide and a carrier; and a polypeptide has the following activities: antilipaemic,
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                                                                                                                                   apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDL;
                                                                                              Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; SEQ ID NO 129; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anantharamiah GM, Garber DW,
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                                                            (first entry)
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                                                            12-AUG-2004
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                                                                                                                                                                                                                                                                      Synthetic.
                       AD034352;
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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymucleocide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E apolipoprotein-E

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 115; 79pp; English.

Datta G;

Garber DW,

WPI; 2004-411629/38. Anantharamiah GM,

(UABR-) UAB RES FOUND

13-NOV-2003; 2003WO-US036268 13-NOV-2002; 2002US-0425821P

WO2004043403-A2.

27-MAY-2004.

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antianginal. The synthetic apolipoproteints maintianginal. The synthetic apolipoproteints maintianginal. The synthetic apolipoproteints maintianginal. The synthetic apolipoproteints maintianginal for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis, and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; molyapetide enhances binding of low-density lipoprotein (IDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
vasotropic, antiarteriosclerotic, cerebroprotective, and
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 AA;
8888888888888888
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Gaps ö 95.9%; Score 94; DB 8; Length 18; 88.9%; Pred. No. 2.6e-07; ive 2; Mismatches 0; Indels 1 GIRRFLGSIWRFIRAFYG 18 Query Match
Best Local Similarity 88.9' ઠે

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1 GIRRFLGSLWRFLRAFYG 18

ADO34340 standard; peptide; 18 AA (first entry) 12-AUG-2004 ADO34340; RESULT 10 ADO34340

apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; seroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL. Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117. 

Synthetic

WO2004043403-A2.

27-MAY-2004

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

Datta G; Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 117; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and apolipoprotein-E mimicking polypeptide and a carrier; and amincking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiatteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

Claim 4; SEQ ID NO 116; 79pp; English.

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antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke, for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
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                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116.
                                                                                                                                                                                                                                  Score 94; DB 8; Length 18; Pred. No. 2.6e-07; Mismatches 0; Indels
                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      ADO34339 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                   1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-NOV-2003; 2003WO-US036268.
                                                                                                                                                                                                                                    95.9%;
88.9%;
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                                                                                                                                                                                                                                                                                                                      1 GIRRFIGSIWRFLRAFYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-AUG-2004 (first entry)
                                                                                                                                                                                                                                                   Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                       Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADO34339;
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uch as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetaliopproteinaemia or atheroscelerosis, and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention. for reducing serum cholesterol in a subject (including a mammal 88999999998888

Sequence 18 AA;

Gaps ö Score 94; DB 8; Length 18; Pred. No. 2.6e-07; 2; Mismatches 0; Indels 18 95.9%; 1 GIRRFLGSIWRFIRAFYG Query Match
Best Local Similarity
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RESULT 12

ADO34297 standard; peptide; 18 AA

ADO34297;

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 74.

(first entry)

12-AUG-2004

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDL;

Synthetic.

WO2004043403-A2.

27-MAY-2004

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P.

(UABR-) UAB RES FOUND

Datta G; Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence

Claim 4; SEQ ID NO 74; 79pp; English

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal 

ô such as a mouse, rat, rabbit, cow, sheap, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalioproteinaemia or atherosaclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein. E minicking apolyapeticide enhances binding of low-density lipoprotein (UDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL, by a cell. This sequence represents a synthetic apolipoprotein. apolipoprotein-E mimicking polypeptide, antilipaemic, cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina, low-density lipoprotein; LDL; very low density lipoprotein; VDDL. Gaps ö Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 21. Score 92; DB 8; Length 18; Pred. No. 5.3e-07; 2; Mismatches 0; Indels 2; Mismatches ΰ mimicking polypeptide of the invention. Datta ADO34244 standard; peptide; 18 AA. 1 GIRRFLGSIWRFIRAFYG 18 GIRKFLGSIWRFIKAFYG 18 Garber DW, 13-NOV-2003; 2003WO-US036268. 13-NOV-2002; 2002US-0425821P 93.9%; 88.9%; Query Match
Best Local Similarity 88.3.
Best Local 16; Conservative 12-AUG-2004 (first entry) (UABR-) UAB RES FOUND. WPI; 2004-411629/38. Anantharamiah GM, WO2004043403-A2 Sequence 18 AA; 27-MAY-2004. Synthetic ADO34244; RESULT 13 AD034244 8888888888888 g

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide and activities: antilipaemic, cardiant, vasotropic, antiarteriosclerocic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal unit including and includin Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, Claim 4; SEQ ID NO 21; 79pp; English.

synthetic apolipoprotein-E mimicking polypeptide is

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chimpanzee or orangutan); for treating coronary artery disease, dysbetalispoproteinsemia or atherosolarosis, and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (IDL) or very low density lipoprotein (VLDL) to a cell and anances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL;
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/note= "All Lys residues are DiMethyl-Lysine"
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                                                                                                                                                                                                  Score 92; DB 8; Leus-Pred. No. 5.3e-07;
                                                                                                                                mimicking polypeptide of the invention.
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88.9%;
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                                                                                                                                                                                                                                                                                       1 GIRRFLGSIWRFIRAFYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity
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                                                                                                                                                                          Seguence 18 AA;
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                        useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chingparzee or oranguran); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein in the subject; polypeptide enhances binding of low-density lipoprotein (UDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 92; DB 8; Length 18;
Pred. No. 5.3e-07;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                         mimicking polypeptide of the invention.
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Best Local Similarity
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useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherescalerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein. E mimicking polypeptide enhances binding of low-density lipoprotein (ULDL) or very low density lipoprotein (ULDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein. E mimicking mimicking polypeptide of the invention. 8x38888888xx

Sequence 18 AA;

ö Gaps ö Query Match
91.8%; Score 90; DB 8; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 1; Indels

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Search completed: May 19, 2006, 14:24:31 Job time : 94.2857 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

May 19, 2006, 14:24:57; Search time 14.2857 Seconds (without alignments) 121.233 Million cell updates/sec Run on:

US-10-712-447-8 98 1 GIRRFLGSIWRFIRAFYG 18

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1000	TOTOG TORSE	hypothetical prote	transcription regu	2-oxoglutarate/mal	poly (3-hydroxybuty	leucyl-tRNA synthe	leucine-tRNA ligas	acriflavin resista	hypothetical prote	0	hypothetical prote	NIP1 protein - yea	TMV resistance pro	reverse transcript	penicillin-binding	ㅁ	cal	hypothetical prote	7)	ce		o-antigen export s		lass I	HLA-A-0	class I	class I	class I hi	ILA-A2.4a ch	gene HLA-A-0205 pr
f	1D	S76462	A75578	G64537	A34341	A84060	H64102	AH3568	T32316	B84733	T33269	A46417	T04583	T12085	E84953	T52113	D72540	T15530	B72692	I54412	F71707	D97700	HLHU69	HLHUA2	I38443	161902	I37542	I84448	18	I38442
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1	Match Length	627	178	461	589	806	861	1025	265	489	516	812	1607	407	760	107	214	228	237	246	258	258	273	365	365	365	365	365	365	365
Query	March	49.0	45.9	44.9	44.9	44.9	44.9	44.4	43.9	43.9	43.9	43.9	43.9	43.4	43.4	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9
	Score	48	45	44	44	44	44	43.5	43	43	43	43	43	42.5	42.5	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42
Result	02	п	7	e	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

transcription regulator, Mark family - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004
C;Accession: A75578
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; P., M.; Shen, M.; Vamathevan, J.G.; Fraser, C.M.
S; Smith, H.O.; Vomter, J.G.; Fraser, C.M.
S; Smith, A.O.; Vomter, J.G.; Fraser, C.M.
S; Smith, H.O.; Vomter, J.G.; Smith, H.O.; Male, M.D.; Male,

45.9%; Score 45; DB 2; Length 178;

Query Match

hypothetical prote leucyl-tRNA synthe leucyl-tRNA synthe leucyl-tRNA synthe leucine-tRNA ligas homolog to drosoph hypothetical prote rap protein - Esc dimethylsulfoxide hypothetical prote control of the leucine rate protein - Esc dimethylsulfoxide hypothetical protein - Esc dimethylsulfoxide hypothetical prote	nypotherical proce probable permease hypotherical prote hypotherical prote hypotherical prote cytochrome P450 DW
T04745. AD1282 AB1583 B89561 B89561 T50337 AG2115 AG2115 C42595 E64109	AF2599 G97381 T08940 F96571 D96776 T02263
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537 803 803 804 790 131 273 359	364 384 503 513
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	444441.8 1.1.4444444.1.8 1.1.8
4 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 4 4
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## ALIGNMENTS

	RESULT 1 S76462  hypothetical protein - Synechocystis sp. (strain PCC 6803) C;Species: Synechocystis sp. A;Variety: PCC 6803 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004 C;Accession: S76462 C;Acc
	A;Reference number: S74322; MUID:97061201; PMID:8905231 A;Accession: S76462 A;Accession: S76462 A;Actual: preliminary A;Molecule type: DNA A;Residues: 1-627 <kan> A;Cross-references: UNIPROT:P74489; UNIPARC:UPIO0000C103F; EMBL:D90915; GB:AB001339; NID:A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996</kan>
· .:	Query Match 49.0%; Score 48; DB 2; Length 627; Best Local Similarity 38.9%; Pred. No. 8.1; Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0; Qy 1 GIRRFLGSIWRPIRAFYG 18  :                     Db 597 GLEQLLGKIWQWLRQKFG 614

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leucyl-tRNA synthetase leuS [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A84060
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and characterium A84060
A;Reference number: A83650, MUID:20512582; PMID:11058132
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acrifilavin resistance protein F (imported) - Brucella melitensis (strain 16M)
acrifilavin resistance protein F (imported) - Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AH3568
R;DelVecchio, V, G.; Kapatral, V,; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P. R;DelVecchio, V, G.; Kapatral, V,; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Lotessc, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; OʻCallaghan, D.; Letessc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fifleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Schence 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.M.; Shith, H.O.; Ven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Status: preliminary
A,Molecule type: DNA
A,Rosidues: 1-806 <-SICO-
A)Rosidues: 1-806 <-SICO-
A)CCOSS-references: UNIPROT: 09K788; UNIPARC: UPI0000136555; GB:AP001518; GB:BA000004; NID:
A,Experimental source: strain C-125
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A;Cross-references: UNIPROT:P43827; UNIPARC:UP1000013655F; GB:U32774; GB:L42023; NID:9157
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C;Superfamily: leucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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Pred. No. 48;
3; Mismatches
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    100 RRFAGDAWRINLPYRFAAAFY 120
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Best Local Similarity 46.2%;
Matches 6; Conservative
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622 GARRFLDRVWRLL 634
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Matches 7; Conservative
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
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J. Bacteriol. 173, 168-175, 1991
A;Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynt
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Datol. Chem. 264, 15298-15303, 1989
A;Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Iden
A;Reference number: A34341; MUID:89359357; PMID:2670936
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A;Accession: A39190
A;Accession: A39190
A;Accession: A39190
A;Accession: A39190
A;Accession: DNA
A;Residues: 1-219 <SCH
A;Cross-references: UNIPARC:UPI000016E162; GB:M64341; NID:g141964; PIDN:AAA21979.1; PID:
A;Note: the authors translated the codon TAC for residue 120 as Thr
C;Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC
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A,Rebidues: 1-589 <REO.
A,Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:g141958; PIDN:
A,Experimental source: strain H16
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C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: G64537
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                                              Gaps
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Pred. No. 26;
2; Mismatches 4; Indels
                                              Indels
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    ed. No. 7.2;
Mismatches
            Pred.
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53.8%;
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297 VRRLLSWFWRFVR 309
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Best Local Similarity 53.8
Matches 7; Conservative
                                              9; Conservative
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A; Residues: 1-461 <TOM>
Best Local Similarity
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                                              Matches
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A;Residues: 1-110,'V',112-582,'O',584-602 <CHU>
A;Cross-references: UNIPARC:UPI0000168ACA; EMBL:Z54141; NID:g1072408; PID:g984682; MIPS:)
A;Experimental source: strain AB972
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N;Alternate names: nuclear import protein; protein YM9924.01c; protein YM9952.11c; protei
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A;Molecule type: DNA
A;Residues: 571-582,'Q',584-640,'K',642,'K',644-812 <CON>
A;Residues: 571-582,'Q',584-640, K',642,'K',644-812 <CON>
A;Cross-references: UNIPARC:UPI0000169ACD; EMBL:Z49212; NID:g798940; PID:g798951; MIPS:YN
R;Churcher, C.M.
submitted to the EMBL Data Library, September 1995
A;Reference number: S59302
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                  P450 homology
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C;Date: 21-Sep-1993 #sequence revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A46417; S539199; S53010
C;Accession: A46417; MUID:93066237; Proc. Natl. Acad. Sci. U.S.A. 89, 10355-10359, 1992
A;Title: NIPl, a gene required for nuclear transport in yeast.
A;Reference number: A46417; MUID:93066237; PMID:1332047
                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-812 <GUI>
A;Residues: 1-812 <GUI>
A;Cross-references: UNIPROT: P32497; UNIPARC: UDI000017B2B1; EMBL: L02899
A;Note: sequence extracted from NCBI backbone (NCBIN:117849, NCBIP:117850)
R;Connor, R.; Churcher, C.M.
submitted to the EMBL Data Library, April 1995
A;Reference number: S53969
                                                                                                                                    Gaps
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A;Map position: 2
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome
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                                                                              Length 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Murray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D. submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid C24B9.
A;Reference number: Z21310
                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein C24B9.13 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: T33269
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                        Score 43; DB 2;
Pred. No. 40;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.9%; Score 43; DB 2;
41.2%; Pred. No. 42;
iive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: CESP:C24B9.13
A;Map position: 5
A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2
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Best Local Similarity 41.2%;
Matches 7; Conservative
                                                                                 43.9%;
54.5%;
                                                                                 Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                6 LGSIWRFIRAF 16
                                                                                                                                                                                                                                                      64
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54 IGNMWSFLRAF
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84733
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PH
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R. Blanchard, M.; Kramer, J.; Elliott, G.; Twyman, B.
submitted to the EMBL Data Library, September 1997
A. Description: The sequence of C. elegans cosmid F31F4.
A. Reference number: Z21149
A. A. Accession: T31316
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: DNA
A. Mesidue: 1-265 cBLA
A. Cross-references: UNIPROT:017136; UNIPARC:UPI000007D19A; EMBL:AF024503; PIDN:AAB70384.
A. Experimental source: strain Bristol N2; clone F31F4
         Proc. Natl. Acad. Sci. U.S.A. 99, 449-440, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-1025 <KUR>
A;Cross-references: UNIPROT:Q8YCQ5; UNIPARC:UPI0000584C8; GB:AE008918; PIDN:AAL53715.1;
A;Experimental source: strain 16M
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A,Introns: 13/3; 67/2
C,Superfamily: Caenorhabditis elegans hypothetical protein T09F5.1
                                                                                                                                                                                                                                                                                                                                                                                                      Length 1025;
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Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 44.4%; Score 43.5; 1
Best Local Similarity 50.0%; Pred. No. 69;
Matches 8; Conservative 4; Mismatches
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   Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
                                                                                                                                                                                                                                                                                                                     A;Map position: II
C;Superfamily: hypothetical protein b2075
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531 FLGSVWSFMTLPRSFF 546
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ilarity 53.8%;
Conservative
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Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-489 <STO>
                                                                                    A; Accession: AH3568
A; Status: preliminary
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4; Mismatches

Query Match Best Local Similarity 53.8%; Matches 7; Conservative

|::| ||||: |: 361 GVKRILGSIFSFV 373 1 GIRRFLGSIWRFI 13

A;Gene: SGD:NIP1 A;Cross-references: SGD:S0004926; MIPS:YMR309c A;Map position: 13R

C;Genetics:

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R;Cormack, R.S.; Hahlbrock, K.; Somssich, I.E.
Plant J. 14, 685-92, 1998
A;Title: Isolation of putative plant transcriptional coactivators using a modified two-hy
A;Reference number: Z25848; MUD:98346011; PMID:9681033
A;Accession: T52113
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                C;Species: Buchnera sp.
C;Adcession: E84953
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. Al
A;Title: Genome sequence of the Nulp:20445173; PMID:10993077
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C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004 C;Accession: T52113
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A;Cross-references: UNIPARC:UPI000005E4C8; GB:AP000398; GSPDB:GN00144
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                                                                                                                                                                                                                            penicillin-binding protein 1b [imported] - Buchnera sp. (strain APS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.4%; Score 42.5; D
44.4%; Pred. No. 74;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: penicillin-binding protein 1B
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||| ||| : |||| |
178 GIRSFLGHVGFYRRFIRDF 196
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Best Local Similarity 50.00.
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Matches 8; Conserv
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A;Gene: KIWI
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A;Molecule type: DNA
A;Cross-references: UNIPROT:O65506; UNIPARC:UPI00000AA45C; EMBL:AL022141
A;Experimental source: cultivar Columbia; BAC clone F23E13
A;Esvan, M.; Wedler, H.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schuelle
submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15418
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C;Species: Vicia faba (fava bean)
C;Accession: T12085
R;Kinoshita, T.; Wada, H.; Masaaki, I.; Shimazaki, K.
submitted to the EMBL Data Library, September 1997
A;Recession: Retrotransposon-like cDNAs from guard cell protoplasts in Vicia faba.
A;Recession: T12085
A;Accession: T12085
A;Accession: T12085
A;Accession: T12085
A;Residues: 1-407 <KIN>
A;Residues: 1-407 <KIN <AIN >
A;Residues: 1-407 <KIN >
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWV resistance protein N homolog F23E13.30 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C; Accession: T94581; T05507 R; Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse, Submitted to the Protein Sequence Database, March 1998 A; Reference number: 215378
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43.9%; Score 43; DB 2; Length 1607;
Best Local Similarity 72.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                            Score 43; DB 2; Length 812;
Pred. No. 66;
                                                                                                                                                                                                                                                                                Indels
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A;Accession: T05507
A;Molecule type: DNA
A;Residues: 1448-1607 - SBE2>
A;Cross-references: UNIPARC:UPI000016DBFD; EMBL:AL022373
A;Experimental source: cultivar Columbia; BAC clone T19K4
C;Genetins:
A;Map position: 4
A;Introns: 193/2; 238/2; 556/2; 930/3; 1029/3; 1287/3
A;Note: F23E13.30; T19K4.270

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RESULT 13

Query Match
43.4%; Score 42.5; D
Best Local Similarity 57.9%; Pred. No. 40;
Matches 11; Conservative 1; Mismatches

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Indels

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DB 2; Length 407;

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Query Match
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                                                                                                                      May 19, 2006, 14:13:32; Search time 115.429 Seconds (without alignments) 144.247 Million cell updates/sec
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                    GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                               2849598 seqs, 925015592 residues
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Q25271_LEPDE
Q9F7V7_RHILV
Q44QD1_CHLLI
Q43K01_9CHLB
Q456F4_9BURS
Q456F4_9BURK
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Maximum Match 100%
Listing first 45 summaries
                                                                                          - protein search, using sw model
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Q8R587
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2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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98
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Match Length
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burkholderi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glavina T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US DOE JOINT GENOME [LARGE SCALE GENOMIC DNA].
US DOE JOINT GENOME INSTITUTE;
COPELAND A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Bryant D., Schmutz J., Larimer F., Land M., Kyrpides N., Ivanova N., Richardson P., "Complete sequence of Chorobium chlorochromatii CaD3.";
Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
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                                           059h73 F
08kby2 c
02y8v4 r
02xw00 m
02s415 c
05cpro d
06llt5 p
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Q25271;
Q25271;
O1-NOV-1996, integrated into UniProtKB/TrEMBL.
O1-NOV-1996, equence version 1.
O1-NOV-1996, entry version 25.
Diapause protein 1 (Fragment).
Name=Dp19;
Leptinotarsa decemlineata (Colorado potato beetle).
Eleptinotarsa decemlineata (Colorado potato beetle).
Eleptinotarsa decemlineata (Colorado potato beetle).
Eleptinotarsa decemlineata (Colorado potato beetle).
Bobtaryota; Metazoa Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
                                                                                                                                                                                                                                                               07vv93
07w7p3
07w131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONT. 2005, integrated into UniProtKB/TrEMBL.
22-NOV-2005, sequence version 1.
21-NOV-2005, sequence version 1.
21-NOV-2006, entry version 5.
21-FBE-2006, entry version 5.
21-FBE-2006, entry version 5.
21-FBE-2006, entry version 5.
21-FBE-2006, contropersion 688;
Chlorobium/Pelodictyon group; Chlorobiales; Chlorobiaceae;
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Pred. No. 3.2;
2; Mismatches 2; Indels
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GO; GO:0005524; F.ATP binding; IEA.
GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   805 AA.
                                                                                           02Y8V4_NITMU
03X4N0_9PRDT
02X415_9SPHI
05CPZ7_CRYPV
08KYR0_DEIRA
06L1T5_PICTO
04BS81_BURVI
07W793_BORPE
07W731_BORPE
07W131_BORPE
                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
     25GH40_BRAKE
                    XKR6 RAT
XKR6 HUMAN
SYL CHLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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622 GISRFLGKVWRFV 634
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les 9; Conservative
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1 GIRRFLGSIWRFIRAF 16
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Q44QD1;
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hes 10, Conservative
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STRAIN=DSM 245;
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NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=290315;
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005684; F:ATP binding; IEA.
GO; GO:0042626; F:ATPase activity; coupled to transmembrane m. . .; IEA.
GO; GO:000166; F:MITPase activity; coupled to transmembrane m. . .; IEA.
GO; GO:0000165; F:incleoride binding; IEA.
GO; GO:0008233; F:protein transporter activity; IEA.
GO; GO:0008565; F:protein transporter activity; IEA.
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                             de Kort C.A.D., Koopmanschap A.B.;
"Nucleotide and deduced amino acid sequence of a cDNA clone encoding
diapause protein 1, an amylphorin-type storage hexamer of the Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhizobium leguminosarum bv. viciae.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.1%; Score 54; DB 2; Length 670; 43.8%; Pred. No. 11; tive 6; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005344; F:oxygen transporter activity; IEA. GO; GO:0006810; P:transport; IEA. InterPro; IPR000896; Hemocyanin. InterPro; IPR005203; hemocyanin. C. InterPro; IPR005204; hemocyanin. C. InterPro; IPR005204; hemocyanin. N. PANTHER; PTHR11511; Hemocyanin, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR 2001, integrated into UniProtKB/TrEMBL 01-MAR-2001, sequence version 1.
7-FBB-2006, entry version 25.
ABC transporter R2cB.
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PROSITE; PS00210; HEMOCYANIN_2; UNKNOWN_1.
                                                                                                                                                                                   potato beetle.";
J. Insect Physiol. 40:527-535(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                   EMBL; X76080; CAA53691.1; -; mRNA.
HSSP; P04253; 1LL1.
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Pfam; PF00372; Hemocyanin_M; 1.
Pfam; PF03722; Hemocyanin_N; 1.
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QF7V7 RHILV PRELIMINARY;
Q9F7V7;
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Best Local Similarity 43.8
Matches 7; Conservative
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                                                                                        NUCLEOTIDE SEQUENCE
                           Leptinotarsa.
NCBI_TaxID=7539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=387;
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Distributed under the Creative Commons Attribution-NoDerivs License
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Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequencing of the draft genome and assembly of Chlorobium limicola DSM 245.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Chlorobium limicola DSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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13-SEP-2006, entry version 9.
Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
CORFNAmes=ClimDRAFT 1980;
CRFOTorbium limicola DSM 245.
Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
Chlorobium/Pelodictyon group; Chlorobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 735
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004823; F:leucine-ERNA ligase activity; IEA.
GO; GO:0006429; P:leucine-ERNA aminoacylation; IEA.
InterPro; PR002302; Leu tRNAByn_la.
PF00133; tRNA-8ynt_l; 1.
GO; GO:0015031; P:protein transport; IEA.
GO; GO:000508; P:proteolysis; IEA.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR0011527; ABC_TM.1.
InterPro; IPR001140; ABC_TM_transpt.
InterPro; IPR003439; ABC_Transpt.
InterPro; IPR003439; ABC_Transpt.
InterPro; IPR003439; ABC_Transplike.
InterPro; IPR00132; Type I sec_HlyB.
PANTHER; PTHR1924:SFT/4; Type_I sec_HlyB; 1.
Pfam; PF00064; ABC_membrans; I.
Pfam; PF00065; ABC_tran; 1.
Pfam; PF00006; ABC_tran; 1.
Prodom; PM00006; ABC_transporter; 1.
Prodom; PM00006; ABC_transporter; 1.
PROSITE; PS00291; ABC_TRANSPORTER; 1.
PROSITE; PS00291; ABC_TRANSPORTER_1; 1.
PROSITE; PS00291; ABC_TRANSPORTER_2; 1.
PROSITE; PS00991; ABC_TRANSPORTER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52; DB 2;
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-SEP-2005, integrated into UniProtKB/TrEMBL
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62.5%; Pred. No. 20,
... 2; Mismatches
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161 GFRWFLPAIWRYRRAF 176
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8 % % S

RESULT 5 Q43K01

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                                                22-NOV-2005, integrated into UniProtKB/TrEMBL.
22-NOV-2005, sequence version 1.
21-FBB-2006, entry version 4.
Hypothetical protein.
OrderedicousNames=Bep18194 A3207;
Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760 / NCIB 9086 / R18194)).
                                                                                                                                                                                                                                                                                                                                                                                                                              US DOE Joint Genome Institute;
Copeland A., iucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M.,
Vergez L., Schmutz J., Larimer F., Land M., Kyrpides N., Lykidis A.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=AU 1054;
US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Annotation of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Burkholderia cenocepacia AU 1054.
Burkholderia; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete sequence of chromosome 1 of Burkholderia sp. 383.";
Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.0%; Score 51; DB 2; Length 407; 47.1%; Pred. No. 20; ive 5; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, CP000151, ABB06809.1, -; Genomic DNA.
Complete protecme: Hypothetical protein.
SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2005, integrated into UniProtKB/TrEMBL. 13-SEP-2005, sequence version 1. 07-FEB-2006, entry version 2. Hypothetical protein.
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407 AA.
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US DOE Joint Genome Institute (JGI-ORNL);
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PRT;
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PRELIMINARY;
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Q456F4;
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                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=269483;
Q39L57_BURS3
Q39L57;
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Matches
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Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
Hammon N., Israni S., genome and assembly of Chlorobium
phaeobacteroides DSM 266.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phaeobacteroides DSM 266.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
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21-FEB-2006, entry version 9.
Leucyl-LRNA synthetase bacterial/mitochondrial, class Ia.
Checyl-LRNA synthetase bacterial/mitochondrial, class Ia.
Chlorobium phaeobacterioides DSM 266.
Bacteria; Chlorobi; Chlorobia; Chlorobianes; Chlorobian/Pelodictyon group; Chlorobium.
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                                                                                                                                                    Query Match 53.1%; Score 52; DB 2; Length 805; Best Local Similarity 61.5%; Pred. No. 29; Matches 8; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=DSM 266;
US DOE JOINT GEOME INSTITUTE (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Chlorobium
                                TIGRFAMB; TIGR00396; leus_bact; 1.
Aminoacyl-tRNA synthetase.
SEQUENCE 805 AA; 91997 MW; D4F3FE28F9E92DF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          816 AA; 93335 MW; 6770B1DAC50560F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AAIB01000002; EAM35935.1; -; Genomic_DNA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
GO; GO:006429; F:leucyl-tRNA aminoacylation; IEA.
InterPro; IPR002302; Leu_tRNAByn_la.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-2005, integrated into UniProtKB/TrEMBL
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PRINTS, PR00985; TRNASNYTHLEU.
TIGRFAMS; TIGR0396; leus_bact; 1.
Aminoacyl-tRNA synthetase.
SEQUENCE 816 AA; 93335 MW: 6777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
      PRINTS; PR00985; TRNASYNTHLEU
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GISRFLGKVWRLV 634
                                                                                                                                                                                                                                                                                                                                          622 GISRFLGKVWRLV 634
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q43K01_9CHLB
Q43K01;
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Q39L57_BURS3
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Gaps

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Name=XKR7; Synonyms=C20orf159, XRG7;
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579 AA;
                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Burkholderia cenocepacia
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                      'Sequencing of the draft genome assembly of Burkholderia cenocepacia
 Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                          STRAIN-HI2424;
US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                   Hypothetical protein.

ORFNames=Bcen2424DRAFT 1071;

Burkholderia cenocepacia H1242.

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                             Score 51, DB 2, Length 408;
Pred. No. 20;
5, Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.0%; Score 51; DB 2; Length 408; 47.1%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
              EMBL; AAHI01000010; EAM12352.1; -; Genomic_DNA.

Hypothetical protein.

SEQUENCE 408 AA; 45545 MW; 3C2BCA9471BAAE93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ll procein.
408 AA; 45603 MW; 7F393888305911D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSGH72 QSNUGS;
11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
07-FBS-2005, sequence version 1.
XK-related protein 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AAHL01000063; EAM16412.1; -; Genomic_DNA.
                                                                                                                                                                                                       02-AUG-2005, integrated into UniProtKB/TrEMBL. 02-AUG-2005, sequence version 1. 07-FEB-2006, entry version 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                579 AA.
                                                                                                                                                                                   408 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                    PRELIMINARY; PRT;
                                                                                                                      328 GIROMLGHVWQWTRSSY 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 GIRQMLGHVWQWTRSSY 344
                                                                                                        1 GIRRFLGSIWRFIRAFY 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GIRRFLGSIWRFIRAFY 17
                                                               Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                 Q4LK44 9BURK
Q4LK44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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XKR7_HUMAN
ID XKR7_HU
AC 05GH72;
DT 11-0CT-
DT 01-MAR-
DT 07-FEB-
UB XK-rela
                                                                                                                                                              RESULT 8
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Distributed under the Creative Commons Attribution-NoDerivs License
             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tracey A., Tromans A.C., Vaudin M., Wait M., Milliams L., Williams S.A., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams L., Williams L., Williams L., Williams L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The DNA sequence and comparative analysis of human chromosome 20.";
Nature 414:865-871(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential).
-!- SIMILARITY: Belongs to the XK family.
-!- CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                         Huang C.-H., Chen Y., "A superfamily of XK-related genes (XRG) widely expressed in "A superfamily of XK-related genes (XRG) widely expressed in vertebrates and invertebrates."; Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 42;
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D8DOFF64B9EDD53D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XK-related protein 7
/FTId=PRO_0000190788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AY534245; AAT07094.1; -; mRNA.
EMBL; AL031658; CAB88102.1; ALT SEQ; Genomic_DNA.
Ensembl; ENSG0000101321; Homo Fapiens.
HGNC; HGNC:23062; XRX7.
Membrane; Transmembrane.
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Potential.
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63826 MW;
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nilarity 58.3%;
Conservative
                                                                                                                      NUCLEOTIDE SEQUENCE [MRNA].
Homo sapiens (Human).
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-!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64302 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.0%;
58.3%;
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190 LGQVWRYLRALY 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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3323
3323
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355
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Best Local Similarity
7; Conserve
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200
303
326
356
356
415
580 AA;
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260
260
303
355
415
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ID XKR7_RAT
AC Q5GH56;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                      Name=XKR7; Synonyms=XRG7;
Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2005, sequence version 1.
07-FBB-2006, entry version 10.
XK-related protein 7.
Name=Xkr7; Synonyms=Xrg7;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chrdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muriaae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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STRAIN=C57BL/6J;
Huang C.-H., Chen Y.;
"A superfamily of XK-related genes (XRG) widely expressed in vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang C.-H., Chen Y.; "A superfamily of XK-related genes (XRG) widely expressed in vertebrates and invertebrates.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6DFE1191093E85D4 CRC64;
                                                                                                                                                         11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
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/FTId=PRO_0000190790.
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Potential
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                                                                                                                     PRT;
                                                                                                                                                                                   13-SEP-2005, sequence version 1.
07-FEB-2006, entry version 6.
XK-related protein 7.
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190 LGQVWRYLRALY 201
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Best Local Similarity 58.3
Matches 7; Conservative
       190 LGQVWRYLRALY 201
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579 AA;
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XKR7_MOUSE
                                                                          RESULT 10
XKR7_PANTR
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07-FBB-2006, entry version 8.
XK-related protein 7.
XK-related protein 7.
XK-related protein 7.
Name=Xkr7; Synonyms=Xrg7;
Rattus norvegicus (Rat).
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Barchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Sprague-Dawley;
Huang C.-H., Chen Y.;
"A superfamily of XK-related genes (XRd) widely expressed in
superfamily of XK-relates ";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-: SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50; DB 1; Length 580;
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential.
F3291FABF4C5A826 CRC64;
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                                                                                                                                                                                                                                                 XK-related protein 7./FTId=PRO_0000190789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2005, integrated into UniProtKB/Swiss-Prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 42;
3; Mismatches
                                                                                                                                            EMBL; AY534253; AAT07102.1; -; mRNA.
Ensembl; ENSMU5600000042631; Mus musculus.
MGL; MGI.3526711; Xkr7.
Membrane; Transmembrane.
(Potential).
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-!- SIMILARITY: Belongs to the XK family.
                                                                                                                                                                                                                                                                                                                                                Potential.
Potential.
Potential.
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Potential.
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Potential.
Potential.
Potential.
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07-FEB-2006, entry version 4.
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NUCLEOTIDE SEQUENCE.
TISSUE=Shoot;
                                                                                                                                                                      NUCLEOTIDE SEQUENCE
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Best Local Similarity
                                                                                                                             NCBI_TaxID=318586;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US DOE Joint Genome Institute (JGI-ORNL); Larimer F., Land M.; Annotation of the draft genome assembly of Burkholderia vietnamiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.,
"Sequencing of the draft genome and assembly of Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina Hammon N., Israni S., Pitluck S., Richardson P.;
Submitted (JAZ-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                       Burkholderia viernamiensis (4.
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, Burkholderia, Burkholderia cepacia complex.
                 Score 50; DB 1; Length 580;
Pred. No. 42;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.0%; Score 49; DB 2; Length 409; Best Local Similarity 41.2%; Pred. No. 42; Matches 7; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypochetical protein.
SEQUENCE 409 AA; 45629 MW; CCD3FA52A9F014E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AAEH02000029; EAM28562.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                    13-SEP-2005, integrated into UniProtKB/TrEMBL.
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                                                                                                                                                                                                                                                              409 AA.
                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                        13-SEP-2005, sequence version 1. 07-FEB-2006, entry version 2. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         329 GVREMLGHVWQWTRSSY 345
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                 58.3%;
                                                                                                                                                                                                                                                                                                                                                                                       ORFNames=Bcep1808DRAFT 3388;
                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                190 LGOVWRYLRALY 201
                                                            7; Conservative
                                                                                                       6 LGSIWRFIRAFY 17
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                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=269482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vietnamiensis G4.
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Q4BFM2;
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Q3PK79 PAR
ID Q3PK7
AC Q3PK7
DT 25-OC
                                                              Matches
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicicae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Paracoccus denitrificans
                                                                                                                                                                                                                                                                                                                   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.; "Sequencing of the draft genome and assembly of Paracoccus denitrificans PD1222."; Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                    Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales,
Rhodobacteraceae, Paracoccus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
SEQUENCE 449 AA; 50659 MW; 5F3EEC9E12AA3B35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD1222."; Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AAIT01000001, EAN68115.1; -; Genomic_DNA. GO; GO: 0020037; F: heme binding; IEA. GO; GO: 00005506; F: irron ion binding; IEA. GO; GO: 0004897; F: meral ion binding; IEA. GO; GO: 0004497; F: monoxygenase activity; IEA. GO; GO: 0006118; P: electron transport; IEA. InterPro; IPR001128; Cycochrome_P450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%; Score 49; DB 64.3%; Pred. No. 46; ative 2; Mismatches
                                                                                                                                                                                                                                                         STRAIN=PD1222;
US DOB Joint Genome Institute (JGI-PGF);
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Cytochrome P450.
ORFNames=PdenDRAFT 4722;
Paracoccus denitrificans PD1222
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9 ROGRGSVWRFIRDF 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00067; p450; 1.
PRINTS; PR00463; EP4501.
PRINTS; PR00385; P450.
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                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
MEDLINE=22417727; PubMed=12529541; DOI=10.1104/pp.012963; Davidson S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.; "The pea gene NA encodes ent-kaurenoic acid oxidase."; Plant Physiol. 131:335-344 (2003).
-!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum (By similarity).
-!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                               EMBL; AF537321; AA023063.1; -; mRNA.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:000506; F:iron ion binding; IEA.

R GO; GO:0006802; F:iron ion binding; IEA.

R GO; GO:0004497; F:monooxygenase activity; IEA.

R GO; GO:0004497; F:monooxygenase activity; IEA.

R GO; GO:0004497; F:monooxygenase activity; IEA.

R GO; GO:0006497; F:monooxygenase activity; IEA.

R GO; GO:0006497; F:monooxygenase activity; IEA.

R PANTHER; PTRN012401; EP4501.

R PANTHER; PR00463; EP4501.

R PRINTS; RR00463; EP4501.

R PRODITE; PS00086; CYTOCHROME P450; UNKNOWN 1.

R Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding; Monooxygenase; Oxidoreductase.

SEQUENCE 488 AA; 56478 MW; 503453CB6E43CB30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 50.0%; Score 49; DB 2; Length 488; Best Local Similarity 58.3%; Pred. No. 50; Matches 7; Conservative 4; Mismatches 1; Indels
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Search completed: May 19, 2006, 14:38:14 Job time : 115.429 secs

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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Baseux, Jean-Louis
APPLICANT: Sexul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Mincher
APPLICANT: Mincher
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
                                              Sequence
Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
US-08-132-767-50
US-08-756-317-5
US-09-134-000C-6620
US-10-360-101-83
US-09-609-146-27
US-09-609-146-29
US-09-538-092-643
US-09-538-092-643
US-08-488-379-3
US-08-488-379-3
US-08-480-190-2
US-08-480-190-2
US-08-480-190-2
US-08-475-399A-2
US-08-480-190-2
US-08-475-399A-2
US-08-475-399A-2
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ZIP: 1036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATIOS SYSTEM: DOS
SOFTWARE: FASTSEN Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 30-743.
APPLICATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
RELEPHONE: 650-493-4935
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-4935
TELEPHONE: GEO-493-5556
TELENTH: BAMIND SEQUENCE THANKER SEGUENCE CHRACTERISTICS:
SEQUENCE CHRACTERISTICS:
SEQUENCE CHRACTERISTICS:
SEQUENCE CHRACTERISTICS:
SEGUENCE CHRACTERISTICS:
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US-08-940-095-242
; Sequence 242, Application US/08940095
; Patent No. 6004925
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6004925e

US-08-940-095-242
                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                               (without alignments)
63.384 Million cell updates/sec
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2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                 May 19, 2006, 14:38:42 ; Search time 24.8571 Seconds
                                                          GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-940-095-242
US-08-940-095-242
US-09-465-719-242
US-09-453-605-242
US-09-453-605-242
US-09-453-818-242
US-09-453-813-242
US-09-453-813-242
US-09-453-813-242
US-09-453-814-242
US-09-453-814-242
US-09-453-899-242
US-09-455-899-242
US-09-455-899-242
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US-09-586-1060-45
US-09-586-1060-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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98
1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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Match
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45.55
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
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US-09-465-719-242
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Jeducace 242, Application US/08940093

Fatent No. 603732

GENERAL INCORANTION:

APPLICANT: Sexual teate the APPLICANT: Sexual teate the APPLICANT: Cornut, Isabelle
APPLICANT: Med., Gunther Gunther General TITLE OF INVENTION: APPLICANTION: APPLICANTION DATA:

COMPUTER: IBM Compatible COMPUTER: PRACE PRACE APPLICANTION DATA:

COMPUTER: APPLICANTION DATA:

APPLICANTION NUMBER: US/08/940,093
FILING DATE: 29-SEP-1997
CLASSIFICANTION NUMBER: BENEROLE POCKET NUMBER: BENEROLE POCKET NUMBER: APPLICANTION NUMBER: BENEROLE POCKET 
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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       Length 18;
                                                                      1; Indels
Query Match
79.6%; Score 78; DB 2; I
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-08-940-096-242
i Sequence 242, Application US/08940096
i Patent No. 6046166
i; GENERAL INFORMATION:
                                                                                                                                     1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                            1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GIRRFLGSIWRFIRAFYG 18
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6037323e
US-08-940-093-242
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US-08-940-093-242
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Contu, Isabelle
APPLICANT: Contu, Isabelle
APPLICANT: Metz, Gunther
ITTLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
ITTLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 242, Application US/09465719

Sequence 242, Application US/09465719

Patent No. 6263377

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Buttner, Klaus

APPLICANT: Buttner, Klaus

APPLICANT: Grant, Isabelle

APPLICANT: Metz, Gunther

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

WUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds Li.P

STREET: 1155 Avern.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: DISKELLE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 30,742
REPERNICE/DOCKET NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REJERNICE/DOCKET NUMBER: 009196-0005-999
TELEPHONE: 650-493-5556
TELEPHONE: 66141 PENNIE
TELERAX: 666-493-4935
TELERAX: 666-493-656
TELERAX: 666-493-656
TELERAX: 666-493-6756
TELERAX: 666-493-6756
TELERAX: 66141 PENNIE
TELERAX: 66141 PENNIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: Pennie & Edmonds LLP
F: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OLECULE TYPE: No. 6046166e US-08-940-096-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: N
COUNTRY:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Beach. Renate
APPLICANT: Sekul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Metz, Jean
ITILE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
ITILE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                           Length 18;
                     REFERENCE/DOCKET NUMBER: 009196-0004-999 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       Query Match 79.6%; Score 78; DB 2; I Best Local Similarity 72.2%; Pred. No. 1.1e-05; Matches 13; Conservative 4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPATRY: USA

ZIP: 10036-2811
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,838
FILING DATE:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
ANME: COLUZZI, LAULEA A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
RECISTRATION NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-4935
                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: NO. 6329341e

SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-453-605-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 242, Application US/09453838
Patent No. 6376464
                                                                        TELEPHONE: 650-493-4935
                                                                                                                                                                                       LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                         TELEPXX: 660-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Cornut, Isabelle
Metz, Guncher
Metz, Guncher
Difourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.6%; Score 78; DB 2; Length 18; 72.2%; Pred. No. 1.1e-05;
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDISKETE
COMPUTER: IDISKETE
COMPUTER: IDISCOMPIDE
OCHARIES
SOFTWARE: FASTSON OF SOFTE
COMPUTER: DOS
SOFTWARE: FASTSON OF SOFTE
CLASSIPTOATION NUMBER: US/09/465,719
FILING DATE:
CLASSIPTOATION DATA:
APPLICATION NUMBER: 08/940,093
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
ANAE: COLUZZI, LAULA A
REGISTRATION NUMBER: 30,742
RECESENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSEN DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,605
FILING DATE: 26-NO. 6329341-1999
CLASSIFICATION CURREN: 08/940,095
PRIOR APPLICATION NUMBER: 08/940,095
FILING DATE: CURROWNATION:
NAME: COTUZZI, LAURA A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-09-453-605-242
; Sequence 242, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                       TELERA: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE SEQ ID NO: 242:
SEQUENCE SEQ ID NO: 242:
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6265377e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 72.23
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: NY
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Sequence 242, Application US/09453841
                                             GENERAL INFORMATION:
                    Patent No. 6573239
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US-09-453-833-242
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                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Backul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
ITILE OF INVENTION: SUPPLY APPROACHES TO
ITILE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
ITILE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
CTITLE OF INVENTION: WE WORK
ADDRESSEE: Pennie & Edmonds LLP
CTITLE OF WAY YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                           Gaps
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                                         Score 78; DB 2; Length 18;
Pred. No. 1.1e-05;
4; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 009196-0007-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER NEGROTAL COMPUTER NEGROTAL STATES DISRECTE COMPUTER: DISRECTE COMPUTER: DISRECTE COMPUTER: DISRECTE COMPUTER: DISREST OF VERSION 2.0 SOFTWARE: FASSED VERSION 2.0 CURRENT APPLICATION NUMBER: US/08/940,136 FILING DATE: 29-SEP-1997 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: FILING DATE: FILING DATE: FILING PARE: COUZZI, LAURA AREJERENCE/DOCKET NUMBER: 30,742 REGISTRATION NUMBER: 30,742 REGISTRATION NUMBER: 009196-00C TELECOMMUNICATION INFORMATION: TELERNONE: 650-493-4935 TELEX: 66141 PENNIE TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 242: CEDITAL COMPANIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                 Sequence 242, Application US/08940136
Patent No. 6518412
                                                                                                                                                          1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GIRRFLGSIWRFIRAFYG 18
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STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6518412e
                                             79.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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Best Local Similarity 72.23
Matches 13; Conservative
                                         Query Match 79.6
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-940-136-242
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    US-09-453-838-242
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Sequence 242, Application US/09453833
Sequence 242, Application US/09453833
Sequence 242, Application US/09453833
Patent No. 660284
GENERAL INFORMATION: Dasseux, Jean-Louis
APPLICANT: Buttner, Klaus
APPLICANT: Gornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gu
                                                                 APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Metz, Met
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CIIY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pennie & Edmonds LLP
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 0091
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-5556
APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GIKKFLGSIWKFIKAFVG 18
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INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: No. 6573239e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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RESULT 8 US-09-453-841-242

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Sequence 242, Application US/09453840
| Sequence 242, Application US/09453840
| Patent No. 6716816
| GENERAL INFORMATION:
| APPLICANT: Dasseux, Jean-Louis
| APPLICANT: Buttner, Klaus
| APPLICANT: Cornut, Isabelle
| APPLICANT: Cornut, Isabelle
| APPLICANT: Dufourcq, Jean
| TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
| TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
| NUMBER OF INVENTION: APOLIPOPROTEIN B-I AGONISTS
| NUMBER OF SEQUENCES: 258
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                 Length 18;
                                                                                                                                                                                                                                                                                                                                                                                               79.6%; Score 78; DB 2; 1
72.2%; Pred. No. 1.1e-05;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEFAX: 650-493-4935
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO: 6630450e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,840
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1155 Avenue of the Americas CITY: New York
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                            US-09-453-826-242
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Difourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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                                                                                                                                                                                                                                          Query Match 79.6%; Score 78; DB 2; I Best Local Similarity 72.2%; Pred. No. 1.1e-05; Matches 13; Conservative 4; Mismatches 1;
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COMPUTER: DEM COMPATION
OPERATING SYSTEM: DOS
SOFTWARE: FASTENCY OVERSION 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/453,826
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                               COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,833
            STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 242, Application US/09453826
Patent No. 6630450
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6602854e
US-09-453-833-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                          CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-453-826-242
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RESULT 14
10S-10-283-599-242
; Sequence 242, Application US/10283599
; Patent No. 6844327
                                                     Sequence 242, Application US/09453834 Patent No. 6753313
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Gornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: No. 6753313e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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                                     US-09-453-834-242
                                                                                                                                                                                                                                                                                                                                                                          STATE: NO COUNTRY:
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Cornut, Isabelle
Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                               Query Match 79.6%; Score 78; DB 2; Length 18; Best Local Similarity 72.2%; Pred. No. 1.1e-05; Matches 13; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.6%; Score 78; DB 2; Length 18; 72.2%; Pred. No. 1.1e-05; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAULE A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: No. 6734169e
SEQUENCE DESCRIPTION: SEQ ID NO: 242:
                                                                                                                                                                                                                                                                                    RESULT 12
US-09-865-989-242
; Sequence 242, Application US/09865989
; Patent No. 6734169
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                      1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
    ; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
TYPE: amino acid
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GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Metz, Gunther
APPLICANT: Metz, G
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APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Difourcq, Jean
TITLE OF INVENTION: GENE THERAPY APPROACHES TO
TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: EM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRAELSCY Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,834
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, LAULA A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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STREET: 1155 Avenue of the Americas
CITY: New York
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Search completed: May 19, 2006, 14:42:55
Job time : 24.8571 secs
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Best Local Similarity 72.2%;
Matches 13; Conservative
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Battner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Cornter, Klaus
APPLICANT: Cornter, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CORTY: New York
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       USE TO TREAT DYSLIPIDEMIC DISORDERS. 274
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Pred. No. 1.1e-05;
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TITLE OF INVENTION: USE TO TREAT DYSLIP1
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
STREET: 1155 Avenue of the Americas
CITY: New York
STAIT: NY
COUNTRY: USA
                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,599
FILING DATE: 29-CT-2002
CLASSIFICATION NUMBER: 08/940,136
PRIOR APPLICATION NUMBER: 08/940,136
PRIOR APPLICATION NUMBER: 30,742
APPLICATION NUMBER: 30,742
ATORNEY/AGENT INFORMATION:
NAME: COTUZZI, LBUTE A
REGISTRATION NUMBER: 009196-000
TELECAMUTNICATION NUMBER: 009196-000
TELECAMUTNICATION NUMBER: 009196-000
TELEPAX: 650-493-5556
TELEFAX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
TTYPE: amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: No. 6844327e
US-10-283-599-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.6%;
Best Local Similarity 72.2%;
Matches 13; Conservative
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Pred. No. 1.1e-05;
4; Mismatches 1; Indels
  APPLICALLE.

FILING DATE: 17-Dec-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
APPLICATION NUMBER: 29-SEP-1997
APPLICATION NUMBER: 30,742
FILING DATE:
ATORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A
FEGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
FILEFAX: 660-493-5566
TELEFAX: 660-493-5566
TELEFX: 6614 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
STAMBEDNESS: single
TYPE: amino acids
STAMBEDNESS: single
TYPE: amino acids
STAMBEDNESS: single
TYPE: MOLECULE TYPE: NO: 6900177e
US-09-465-718-242
APPLICATION NUMBER: US/09/465,718 FILING DATE: 17-Dec-1999
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Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database

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US-10-712-447-2

US-10-712-447-2

Sequence 2, Application US/10712447

Sequence 2, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANATHERARIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYBEPTIDES MIMICKING

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

FILE REFERENCE: 11273-1234

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT APPLICATION NUMBER: G0/425,821

FRIOR FILING DATE: 2002-11-13

FRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENTIN VET: 3.2

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-10-712-47-5
US-10-712-47-5
Sequence 5, Application US/10712447
Publication No. US20040186057A1
GENERAL INFORMATION:
APPLICANT: GARBER, DAVID W.
APPLICANT: GARBER, DAVID W.
TITLE OF INVENTION: SYNCHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING;
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE;
TILE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE;
CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
                                                                   Sednence
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide FEATURE:
COTHER INFORMATION: c-term amidated US-10-712-447-2
 Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 98; DB 4; Length 18; 100.0%; Pred. No. 9.8e-08; tive 0; Mismatches 0; Indels
US-10-712-447-22
US-10-712-447-78
US-10-712-447-195
US-10-712-447-19
US-10-712-447-19
US-10-712-447-58
US-10-712-447-77
US-10-712-447-79
US-10-712-447-79
US-10-712-447-94
US-10-712-447-97
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ORGANISM: Artificial Sequence
-FEATURE:
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Best Local Similarity
   885.7
885.7.7
8833.7.7.7
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882.7.7
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Sequence 5, Appli
Sequence 10, Appli
Sequence 11, Appl
Sequence 115, Appl
Sequence 117, Appl
Sequence 117, Appl
Sequence 117, Appl
Sequence 131, Appl
Sequence 121, Appl
Sequence 114, Appl
Sequence 113, Appl
Sequence 113, Appl
Sequence 114, Appl
Sequence 114, Appl
Sequence 117, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                       GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-712-447-6
US-10-712-447-10
US-10-712-447-11
US-10-712-447-11
US-10-712-447-11
US-10-712-447-11
US-10-712-447-11
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US-10-712-447-11
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                                                                                                                                                                                                                                                                                                              2097797 seqs, 463214858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                                                          US-10-712-447-8
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Match Length
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Result

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Gaps

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US-10-712-447-10
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APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: GARBER, DAVID W.
TOTLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT FILING DATE: 2003-11-13
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PATENTIN VET. 3.2
SOFTWARE: PATENTIN VET. 3.2
SEQ ID NO 8
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:
APPLICANT: GARBER, DAVID W.
APPLICANT: GARBER, DAVID W.
APPLICANT: DATTA, GERTA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
TITLE OF INVENTION APOLIPOPROTEIN E AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210
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                                                                                                                                                                                                            ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-10-712-447-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 98; DB 4; Length 18; Best Local Similarity 100.0%; Pred. No. 9.8e-08; Matches 18; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 60/425,821
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 5
LENGTH: 18
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Publication No. US20040186057A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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US-10-712-447-10
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US-10-712-447-8
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                                                                                                                                                    TYPE: PRT
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| Sequence 91, Application US/10712447
| Publication No. 120040186057A1
| GENERAL INFORMATION:
| APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
| APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
| APPLICANT: DATTA, GEETA
| TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
| TITLE OF INVENTION: APPLICANTION: APPLICANTION APPLICANTION APPLICANTION APPLICANTION NUMBER: US/10/712,447
| CURRENT APPLICATION NUMBER: US/10/712,447
| PRIOR APPLICATION NUMBER: 60/425,821
| PRIOR APPLICATION NUMBER: 60/425,821
| PRIOR APPLICATION NUMBER: 60/425,821
| SAOFTWARE: PALENT OF SEQ ID NOS: 210
| SOFTWARE: PALENT OF SEQ ID NOS: 210
| SEQ ID NO 91
| LENGTH: 18
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-10-712-447-13
Squence 13, Application US/10712447
Squence 13, Application US/10712447
Squence 13, Application US/10712447
Squence 13, Application US. 10712447
Squence 13, Application US. 10806057A1
GRENERAL INFORMATION:
APPLICANT: APPLICANT: DATTA, GEETA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APPLICANCE: 112739-12308
CURRENT APPLICATION WHORER: US/10/712,447
CURRENT FILING DATE: 2003-11-13
PRIOR FILING DATE: 2003-11-13
PRIOR FILING DATE: 2002-11-13
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                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                  100.0%; Score 98; DB 4; 100.0%; Pred. No. 9.8e-08; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 98; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0;
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                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 10
LENGTH: 18
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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 13
LENGTH: 18
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Best Local Similarity 100.
Matches 18; Conservative
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US-10-712-447-129
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US-10-712-447-117
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Sequence 116, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: MANTHARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

FILE REFERENCE: 112739-1230S

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT PILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

FRIOR FILING DATE: 202-11-13

SEQ ID NO 116

LENGTH: 18

LENGTH: 18

LENGTH: 18
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1 Sequence 115, Application US/10712447

1 Publication No. US20040186057A1

2 FORDERL INFORMATION:

3 APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

3 APPLICANT: DATTA, GEETA

5 TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

5 TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

7 TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

7 TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

7 TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

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7 TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

7 TITLE OF INVEN
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                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic JOTHER INFORMATION: peptide US-10-712-447-91
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ORGANISM: Artificial Sequence
FEATURE:
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TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                   FEATURE:
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Sequence 117, Application US/10712447

Sequence 117, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANATHARAMIAH, GATTADAHALLI M.

APPLICANT: GARBER, DAVID W.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

FILE REFERENCE: 11273-1230

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT PILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

FRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENTING VET. 3.2

LENGTH: 18
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Publication No. US20040186057A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: DATTA, GEETA
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILE REPRENCE: 112799-123US
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT APPLICATION NUMBER: 06/425,821
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 129
LERGTH: 18
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; COTHER INFORMATION: peptide US-10-712-447-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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                                                                                                            Length 18
                                                                                                      Score 94; DB 4; I
Pred. No. 3.9e-07;
2; Mismatches 0
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
                                                                                                         Query Match 95.9%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
  Mismatches
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                                           1 GIRRFLGSIWRFIRAFYG 18
                                                                                        1 GIRRFLGAIWRFIRSFYG 18
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Best Local Similarity 88.9%;
Matches 16; Conservative ;
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  16; Conservative
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NAME/KEY: MOD_RES
LOCATION: (3)
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LOCATION: (14)
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US-10-712-447-74
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                                                                                                                                                                                                                                                               Sequence 131, Application US/10712447

| Sequence 131, Application US/10712447
| Publication No. US20040186057A1
| GENERAL INFORMATION:
| APPLICANT: ANANTHARATAN, GATTADAHALLI M.
| APPLICANT: GARBER, DAVID W.
| TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
| TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
| TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
| TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
| TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
| TITLE OF INVENTION UNMBER: 60/425,821
| PRIOR APPLICATION NUMBER: 60/425,821
| PRIOR PELING DATE: 2002-11-13
| NUMBER OF SEQ ID NOS: 210
| SEQ ID NO 131
| LENGTH: 18
| LENGTH: 18
| TYPE: PRT
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Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: BATTA, GETA

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

FILE REFERENCE: 12739-1239

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT PILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER: OF SEQ ID NOS: 210

SOFTWARE: Patentin Ver. 3.2

LENGTH: 18
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US-10-712-447-131
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US-10-712-447-21
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Pred. No. 7.9e-07;
                       Length 18;
                                                                     0; Indels
                     Score 94; DB 4; I
Pred. No. 3.9e-07;
2; Mismatches 0
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88.94;
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ORGANISM: Artificial Sequence
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                     Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity
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US-10-712-447-53

Sequence 53, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHARAMIH, GATTADAHALLI M.

APPLICANT: ANANTHARAMIH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT PAPLICATION NUMBER: 60/425,821

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENTIN VET: 3.2

SEQ ID NO 53

LENGTH: 18
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APPLICANT: ARABER, DAVID W.
APPLICANT: DATTA, GEETA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILE REFERENCE: 112739-123US
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT APPLICATION NUMBER: 06/425,821
PRIOR PELLING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PALENTIN Ver. 3.2
SOFTWARE: PALENTIN Ver. 3.2
LENGTH: 18
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Gaps
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US-10-712-447-4

i Sequence 4, Application US/10712447

sequence 4, Application US/10712447

spublication No. US20040186057A1

j GENERAL INFORMATION:
    APPLICANT: ANATHARAMIAH, GARTADAHALLI M.
    APPLICANT: DATTA, GEETA
    ITILE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
    TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
    TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
    TICRERT APPLICATION NUMBER: US/10/712,447
    CURRENT PILING DATE: 2003-11-13
    PRIOR FILING DATE: 2003-11-13
    PRIOR FILING DATE: 2002-11-13
    PRIOR FILING DATE: 2002-11-13
    SEQ ID NO 4
    LENGTH: 18
    TYPE: PRT
    CRANISM: Artificial Sequence
    PEATURE APPLICATION NUMBER: COMPANIENT ON THE OFFICE OFFIC
                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                       Query Match
93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels
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91.8%; Score 90; DB 4; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e-06;
Matches 17; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                        1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GIRKFLGSIWRFIKAFYG 18
; OTHER INFORMATION: peptide US-10-712-447-74
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Search completed: May 19, 2006, 15:27:57 Job time : 81.2857 secs

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Sequence 2947, Ap
Sequence 118, Appl
Sequence 111, Appl
Sequence 5, Appli
Sequence 2540, Ap
Sequence 240, Ap
Sequence 27, Appli
Sequence 109, Appli
Sequence 109, Appli
Sequence 109, Appli
Sequence 40, Appli
Sequence 40, Appli
Sequence 40, Appli
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853, App
40, Appl
12, Appl
336, App
169, App
137, App
1, Appli
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| EMC_Celerra SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
| FMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaad/US07_NEW_PUB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaad/PCT_NEW_PUB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaad/US08_NEW_PUB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaad/US10_NEW_PUB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaad/US10_NEW_PUB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaad/US10_NEW_PUB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaad/US10_NEW_PUB.pep:*
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17.943 Million cell updates/sec
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-949-925-111
US-11-302-505A-8
US-11-242-505A-8
US-10-511-937-2540
US-10-975-928-543
US-11-169-140-109
US-11-204-427-7
US-11-304-129-40
US-11-304-129-40
US-11-505-928-545
US-10-505-928-545
US-10-505-928-645
US-10-505-928-640
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US-11-204-427-1
US-10-196-749-274
US-11-251-465-18
US-11-261-384-2
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US-10-196-749-336
US-11-024-544A-169
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Maximum Match 100%
Listing first 45 summaries
                                                                                               - protein search, using sw model
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98
1 GIRRFLGSIWRFIRAFYG 18
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Maximum DB seq length: 200000000
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No.
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16, Appl
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APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Prentice, James
APPLICANT: Prentice, James
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PATENTIN VERSION 3.2
SOFTWARE: PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 441;
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US-11-223-738-6
US-11-324-548-18-18-11-190-750-135
US-11-190-750-135
US-11-264-784-87
US-11-264-784-87
US-10-541-993-26
US-10-561-993-26
US-11-351-664-44
US-11-257-662-44
US-11-257-664-46
US-11-257-664-46
US-11-257-664-46
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                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                            RESULT 1:937-2947
US-10-511:937-2947
US-quence 2947, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-242-505A-18
Sequence 18, Application US/11242505A
Bublication No. US20060099656A1
GENERAL INFORMATION:
APPLICANT: Carroll, Joseph M.
RAPLICANT: Healy, Aileen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 GLSKFLGTHWLMGNILRLLFG 126
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  ) ORGANISM: Homo sapiens
US-10-511-937-2947
   RESULT 2
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RESULT 5
US-11-302-678-5
Sequence 5, Application US/11302678
Sequence 5, Application WS/11302678
Publication No. US2006008881A1
GENERAL INFORMATION:
APPLICANT: Allos-Santiago, Inmaculada
APPLICANT: Venkateswarlu, Karicheti
TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: UROLGGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
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                                                                                                          7;
Score 36.5; DB 1; Length 60;
Pred. No. 2.2;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: 67 Human secreted proteins
TITLE OF INVENTION: 67 Human secreted proteins
FILE REFERENCE: PO13P2
CURRENT APPLICATION NUMBER: US/09/949,925
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 60/232,150
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 111, Application US/09949925
Publication No. US20060099575A9
GENERAL INFORMATION:
             Query Match 37.2%;
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                              5 FLGSIWRFIRAFYG 18
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31 FLILVWIFV-AFYG 43
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 6; Conserv
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    TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 14717, 9941, 19310,
FILE REPERENCE: MPISO101-288PIRCPLOWNIN
CURRENT FILING DATE: 2005-10-03
FRIOR PELING DATE: 2005-10-03
FRIOR PELING DATE: 2002-11-07
FRIOR PELING DATE: 2001-11-07
FRIOR PELING DATE: 2001-11-07
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FRIOR PELING DATE: 2001-11-07
FRIOR FILING DATE: 2001-12-17
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37.8%; Score 37; DB 7; Length 403;
Best Local Similarity 55.6%; Pred. No. 16;
Matches 5; Conservative 3; Mismatches 1; Indels
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Publication No. US20060099575A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 67 Human secreted proteins
FILE REFERENCE: PZ023P2
CURRENT FILING DATE: 2001-09-12
PRIOR FILING DATE: 2000-12-09
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-01-37
PRIOR FILING DATE: 1999-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR PLING DATE: 1998-01-30
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NAME/KEY: SITE

LOCATION: (60)

OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-142
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-242-505A-18
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CURRENT APPLICATION NUMBER: US/11/302,678

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GENERAL INCOMPATION:

APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION

APPLICANT: Browse, John A

APPLICANT: Watts, John A

APPLICANT: Watts, John A

APPLICANT: Watts, Johnifer L.

TITLE OF INVENTION: POLYUNSAURATED FATTY ACIDS

TITLE OF INVENTION: POLYUNSAURATED FATTY ACIDS

TITLE OF INVENTION: POLYUNSAURATED FATTY ACIDS

TILE REFERENCE: 4630-58963-02

CURRENT APPLICATION NUMBER: US/10/975,692

CURRENT PALING DATE: 2004-10-26

FRIOR PALICATION NUMBER: PCT/US99/28655

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PARCHINI VERSION 3.3

SSEQ ID NOS: 17
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APPLICANT: Prentice, James
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: ROSenberg, Steven
TITLE OF INVENTION: MAD MONITORING TRANSPLANT REJECTION
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REPRENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR PELLING DATE: 2003-04-24
PRIOR PELLING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR PELLING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PALENTIN VERSION 3.2
SOFTWARE: PALENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 6; Length 351;
Pred. No. 44;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                               APPLICANT: EXPRESSION DIAGNOSTICS, INC
                                                                                                                                                                                                           Sequence 2540, Application US/10511937 Publication No. US20060088836A1 GENERAL INFORMATION:
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Publication No. US20060090221A1
GENERAL INFORMATION:
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; ORGANISM: Caenorhabditis elegans
US-10-975-692-2
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Fry, Kirk
Woodward, Robert
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| | |: |||
195 LEEAWSFLDAFY 206
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Best Local Similarity
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APPLICANT: Carroll, Joseph M.
APPLICANT: Healy, Aileen
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 222, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
FILE REFERENCE: MPIZO01-288PIRCPHOMNIM
CURRENT APPLICATION NUMBER: US 11/242,505A
CURRENT APPLICATION NUMBER: US 10/290,078
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-17
SRIOR APPLICATION NUMBER: G6/341,606
PRIOR FILING DATE: 2001-12-16
PRIOR APPLICATION NUMBER: G6/341,606
PRIOR FILING DATE: 2001-12-16
PRIOR FILING DATE: 2001-12-16
PRIOR FILING DATE: 2001-12-16
PRIOR PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 36.7%; Score 36; DB 7; Length 599; Best Local Similarity 71.4%; Pred. No. 38; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                  PRIOR FILING DATE: 2003-01-18
PRIOR FILING DATE: 2003-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-08-14
PRIOR PILING DATE: 2002-08-14
PRIOR PILING DATE: 2002-08-14
PRIOR PILING DATE: 2002-08-14
PRIOR FILING DATE: 2002-08-1
PRIOR PRILING DATE: 2002-10-21
PRIOR PRILING DATE: 2002-11-05
PRIOR PILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 66
SOTWARE: PASESEQ FOR WINDOWS VERSION 4.0
SEQ ID NOS: 66
                                                                            PRIOR APPLICATION NUMBER: US/10/345,680 PRIOR FILING DATE: 2003-01-16
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; Sequence 48, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo Sapiens
US-11-302-678-5
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64 LGNVWRF 70
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Sequence 40. Application US/11304129
; Publication No. US20060088915A1
GENERAL IRPORANTION:
GENERAL IRPORANTION:
APPLICANT: WASUDA, Yasushi
APPLICANT: WATANABE, Takuya
APPLICANT: TERACHY, Yoshihiro
APPLICANT: TERACHY, Yasushi
APPLICANT: TERACHY, Yasushi
APPLICANT: TERACHY, Yasushi
APPLICANT: TERACHY, Yasushi
APPLICANT: MATANABE, Takuya
APPLICANT: MATANABE, Takuya
APPLICANT: MATANABE, USAUJA
APPLICANT: MATANABE, USAUJA
APPLICANT: HINUMA, Syuji
APPLICANT: HINUMA, Syuji
APPLICANTION NUMBER: US/11/304,129
CURRENT FILING DATE: 2005-12-15
FRIOR APPLICATION NUMBER: US/10/333,192
FRIOR PRILING DATE: 2000-07-18
FRIOR APPLICATION NUMBER: UP 2001-26779
FRIOR APPLICATION NUMBER: UP 2001-26779
FRIOR APPLICATION NUMBER: PCT/JP01/06162
FRIOR APPLICATION NUMBER: PCT/JP01/06162
FRIUM APPLICATION NUMBER: PCT/JP01/06162
FRIUM APPLICATION NUMBER: PCT/JP01/06162
FRIUM SEQ ID NOS: S8
FROW FILING DATE: 2001-07-17
FROWTH ON 40
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                        Length 244;
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Pred. No. 75;
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                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/11204427;
Publication No. US20060100146A1
GENERAL INFORMATION:
APPLICANT: Sturley, Stephen I.
APPLICANT: Bilheimer, Jeffrey T.
APPLICANT: Cromley, Debar I.
ANGREN APPLICATION NUMBER: US/11/204,427
CURRENT FILING DAGE: 73
SOFTWARE: PatentIn version 3.3
                              DB 7;
                        Query Match
34.2%; Score 33.5; D
Best Local Similarity 42.1%; Pred. No. 35;
Matches 8; Conservative 3; Mismatches
                                                                                                                                                                                                          158 GLVLALGAVWCVARARFIR 176
                                                                                                                                               1 GIRRFLGSIW----RFIR 14
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Matches 5, Conservative
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84 AIWRQLRDYY 93
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Best Local Similarity
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ORGANISM: Rat
US-11-304-129-40
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US-11-304-129-40
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US-11-204-427-7
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Sequence 109, Application US/11169140
Sequence 109, Application US/11169140
Sublication No. US20060099150A1
SABLICANT: NUCRAMATION:
APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
APPLICANT: HAWLEY, Stephen
APPLICANT: MUNGER: US/11/169,140
CURRENT FILING DATE: 2005-06-20
FILE REFERENCE: 1144-037-999
CURRENT FILING DATE: 2006-11-13
PRIOR PPLICATION NUMBER: US 60/248,478
PRIOR APPLICATION NUMBER: US 60/249,039
PRIOR PPLICATION NUMBER: US 60/249,039
PRIOR PLING DATE: 2001-00-02
PRIOR PLING DATE: 2001-10-02
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Query Match 34.7%; Score 34; DB 6; Length 447; Best Local Similarity 43.8%; Pred. No. 59; Matches 7; Conservative 4; Mismatches 5; Indels
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Pred. No. 70;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                     Sequence 543, Application US/10505928
; Publication No. US2006008532A1
; GENERAL INFORMATION: US2006008532A1
; APPLICANT: Ludwig Institute for Cancer Research
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/3917
; FILE REFERENCE: 28967/3917
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; SEQ ID NOS: 866
; SGTWARE: PARENTIN 3.2
; LENGTH: 522
; TYPE: PRI
; ORGANISM: Homo sapiens
US-10-505-928-543
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130 IRKILETIFTILFAFY 145
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Best Local Similarity 47.1%;
Matches 8; Conservative
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US-10-505-928-543
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RESULT 15
US-10-565-928-853
; Sequence 853, Application US/10505928
; Publication No. US2006008832A1
; Publication No. US2006008833A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; TITLE APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR FILING DATE: 2002-03-07
; NUMBER 0F SEQ ID NOS: 866
; SOFTWARE: Patentin 3.2
; SEQ ID NO 853
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339 RYYSSEYHYVGGFYG 353
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Best Local Similarity 50.0%;
Matches 6; Conservative
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1122 LGLIYFFVQRFY 1133
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ORGANISM: Homo sapiens
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Sequence 48, Application US/11304129

Publication No. US20066088915A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MASUDA, Yasushi
APPLICANT: TAKATSU, Yoshihiro
APPLICANT: TAKATSU, Yoshihiro
APPLICANT: TERAO, Yasushi
APPLICANT: TERAO, Yasushi
APPLICANT: HINDAA, Syuji
I APPLICANT: HINDAA, Syuji
I APPLICANT: HINDAA, Syuji
I TILE OP INVENTION: NOVEL Physiologically Active Peptide and Use Thereof
FILE REFERENCE: 2762USOP
CURRENT FILING DATE: 2003-02-29
FRIOR FILING DATE: 2003-02-29
FRIOR FILING DATE: 2000-07-18
FRIOR FILING DATE: 2001-07-18
FRIOR FILING DATE: 2001-07-18
FRIOR FILING DATE: 2001-07-18
FRIOR FILING DATE: 2001-07-18
FRIOR FILING DATE: 2001-07-17
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33.7%; Score 33; DB 6; Length 463;
Best Local Similarity 33.3%; Pred. No. 90;
Matches 5; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 7; Length 393;
Pred. No. 75;
1; Mismatches 6; Indels
     Indels
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TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR PELING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARER: PALENTIN 3.2
ENG ID NO 545
LENGTH: 463
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 545, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 46.2%;
Matches 6; Conservative
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                                                                                                      216 PCGQIWPVDQQPY 228
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                                                        5 FLGSIWRFIRAFY 17
     6; Conservative
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US-10-505-928-545
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        Matches
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4 RFLGSIWRFIRAFYG 18

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Gaps

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Score 33; DB 6; Length 1531; Pred. No. 3.6e+02; 3; Mismatches 3; Indels

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Run

geneseqp20028:\* geneseqp2003as:\* geneseqp2006s:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp2005s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2 2 2 2 5 6 5	7 8 8 6	2 H M M	1 60 60 1 4 70 70	3 B B 2 C	4 4 4 0 11 0	4 4 4 6 4 8

## ALIGNMENTS

RESULT 1

summaries

geneseqp1980s:\*

A Geneseq\_8:\* 1: geneseqp19

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Database

Post-processing: Minimum Match 1008 Maximum Match 1008 Listing first 45 su

apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina: low-density lipoprotein; LDL; very low density lipoprotein; UDL; Synthetic apolipoprotein-E mimicking paptide, SEQ ID No 8. ADO34231 standard; peptide; 18 AA. (first entry) WO2004043403-A2 12-AUG-2004 Synthetic ADO34231; AD03423 

27-MAY-2004.

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P.

(UABR-) UAB RES FOUND.

ဗ် Datta Garber DW, Anantharamiah GM,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 8; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypeptide and a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic

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apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and cardiant, rhe synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal cuthing serum cholesterol in a subject (including a mammal cuthing serum crosserol in a subject (including a mammal chimperate or orangutuan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking colypeptide enhances binding of low-density lipoprotein (ULDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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Sequence 18 AA;

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Gaps
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0
100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 6.4e-08;
                     0; Indels
                       0; Mismatches
                                                           1 GIRRFLGSIWRFIRAFYG 18
                       18; Conservative
            Local Similarity
 Query Match
                       Matches
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Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide ADO34225 standard; peptide; 18 AA. (first entry) 12-AUG-2004 ADO34225; 

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholestreol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

Synthetic.

'note= "N-terminal acetyl" Location/Qualifiers /note= "C-terminal Key Modified-site Modified-site

WO2004043403-A2

27-MAY-2004

13-NOV-2002; 2002US-0425821P.

13-NOV-2003; 2003WO-US036268

(UABR-) UAB RES FOUND

Anantharamiah GM, Garber DW,

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. WPI; 2004-411629/38.

Datta G;

Claim 4; SEQ ID NO 2; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

WPI; 2004-411629/38.

ID NO 5; 79pp; English.

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c a host cell, a recombinant cell or a transgenic, non-human subject

(including animal or plant) comprising the synthetic apolipoprotein-E

minicking polypeptide encoding polymicleotide, a composition comprising

the synthetic apolipoprotein-E minicking polypeptide and a carrier; and

an monoclonal antibody that specifically binds to the synthetic

an encolonal antibody that specifically binds to the synthetic

an encolonal antibody that specifically binds to the synthetic

and alpoprotein-E minicking polypeptide. The synthetic apolipoprotein-E

cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

antianginal. The synthetic apolipoprotein-E minicking polypeptide is

cardiant, vasotropic, antiarteriosclerotic, pig, human, monkey, apc,

cardiant, pror reducing serum cholesterol in a subject (including a mammal)

cuch as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, apc,

chimpanzee or orangutan); for treating coronary artery disease,

chimpanzee or orangutan); for treating coronary artery disease,

chocardial infarction or stroke; for breaking an embolus in the subject;

and also for treating angina. The synthetic apolipoprotein-E minicking

colypeptide enhances binding of low-density lipoprotein (IDL) or very low

density lipoprotein (VLDL) to a cell and enhances degradation of LDL or

vLDL by a cell. This sequence represents a synthetic apolipoprotein-E

minicking polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 AA;
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ADO34228
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mimicking polypeptide encoding polynucleotide; a composition comprising
the synthetic apolipoprotein-B mimicking polypeptide and a carrier; and
an monocolonal antibody that specifically binds to the synthetic
apolipoprotein-B mimicking polypeptide. The synthetic apolipoprotein-E
cardiant, vasotropic, antiarteriosclerotic, cerebroprotecilve, and
antianginal. The synthetic apolipoprotein-B mimicking polypeptide is
useful for reducing serum cholesterol in a subject (including a mammal
used as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
chimpanzee or orangutan); for treating coronary artery disease,
chimpanzee or orangutan); for treating coronary artery disease,
dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
myocardial infarction or stroke; for breaking an embolus in the subject;
and also for treating angina. The synthetic apolipoprotein-B mimicking
polypeptide enhances binding of low-density lipoprotein (LDL) or very low
density lipoprotein (VLDL) to a cell and enhances degradation of LDL or

VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.

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Gaps

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0; Indels

100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 6.4e-08;

0; Mismatches

18; Conservative

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Query Match Best Local Similarity

Sequence 18 AA;

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(including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbecalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject;
                                                                                                                                                                                                                                                                                                                     and also for treating angina. The synthetic apolipoprotein-E mmircking polypeptide enhances binding of low-density lipoprotein (LDL) or very lc density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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Best Local Similarity 100.0
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Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
                                                                                   apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholestrent, coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDL.
                                                             Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 13.
                                                                                                                                                                                                                                                                                                                           Anantharamiah GM, Garber DW, Datta G
                                                                                                                                                                                                                                               13-NOV-2003; 2003WO-US036268
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                                    12-AUG-2004 (first entry)
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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E

Claim 4; SEQ ID NO 13; 79pp; English.

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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
                                                                                                                                                              apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL;
                                                                                                                                Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Datta G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; SEQ ID NO 10; 79pp; English.
                               ADO34233 standard; peptide; 18 AA
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                                                                                                  (first entry)
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                                                                                                    12-AUG-2004
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                                                                                                                                                                                                                                                                        Synthetic
                                                                  ADO34233;
AD034233
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the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antiargainal. The synthetic apolipoprotein-E mimicking polypeptide is untianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for breaking and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide of the invention.

"Und. by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
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Sequence 18 AA;

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Gaps
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100.0%; Score 98; DB 8; L
100.0%; Pred. No. 6.4e-08;
iive 0; Mismatches 0;
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1 GIRRFLGSIWRFIRAFYG 18

ADO34314 standard; peptide; 18 (first entry) 12-AUG-2004 AD034314; RESULT 6 AD034314 

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Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 91.

vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dybbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL. apolipoprotein-B mimicking polypeptide; antilipaemic; cardiant;

Synthetic

WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. WPI; 2004-411629/38.

Datta G;

Anantharamiah GM, Garber DW,

Claim 4; SEQ ID NO 91; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

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an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal companze or orangutan); for treating coronary artery disease, chimpanze or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking colypeptide enhances binding of low-density lipoprotein (UDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or wishing a cell. This sequence represents a synthetic apolipoprotein-E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypeotide, a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDL;
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                                                                                                                                                                                                                                                                                         mimicking polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADO34354 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GIRRFLGSIWRFIRAFYG
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                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 94.4 es 17; Conservative
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                                                                                                                                                                                                                                                                                                                                Sequence 18 AA;
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Matches
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Gaps

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Score 94; DB 8; Length 18; Pred. No. 2.6e-07; 2; Mismatches 0; Indels

95.9%;

Query Match Best Local Similarity

Sequence 18 AA;

2; Mismatches

16; Conservative

Matches

18 18

1 GLRRFIGSIWRFIRAFYG 1 GIRRFLGSIWRFIRAFYG

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such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for treating coronary artery disease, my disease, and such a subject is an also for reating and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.

cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal

mimicking polypeptide has the following activities: antilipaemic,

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          minicking polypeptide has the following activities: antilipaenic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein: E minicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (ULD) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E minicking minicking polypeptide of the invention.
 polypeptide. The synthetic apolipoprotein-E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
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                                                                                                                                                                                                                                                                                   Score 94; DB 8; Length 18; Pred. No. 2.6e-07;
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                                                                                                                                                                                                                                                                                   95.9%;
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mimicking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                   Query Match 95.9
Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                                                                  Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
                                                                                                                                                                                      apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL;
                                                                                                                                                      Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Datta G;
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                                    ADO34352 standard; peptide; 18 AA
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                                                                                                                 (first entry)
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                                                                            AD034352;
                      ADO34352
RESULT
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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polyperide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E

Claim 4; SEQ ID NO 115; 79pp; English.

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cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synchetic apolipoprotein-E minicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E minicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E minicking polypeptide of the invention.
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Sequence 18 AA;

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95.9%; Score 94; DB 8; Length 18;
88.9%; Pred. No. 2.6e-07;
ive 2; Mismatches 0; Indels
                                                                                        1 GIRRFLGSIWRFIRAFYG 18
Query Match
Best Local Similarity 88.>°,
Best Local Similarity
Best Local Similarity
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Gaps

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1 GIRRFLGSLWRFLRAFYG 18 용

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117. ADO34340 standard; peptide; 18 AA. 12-AUG-2004 (first entry) ADO34340; RESULT 10 ADO34340 

apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholestrenl; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina: low-density lipoprotein; LDL; very low density lipoprotein; UDL;

Synthetic

WO2004043403-A2.

27-MAY-2004

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P.

(UABR-) UAB RES FOUND

Datta G; Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 117; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide are a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic and apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

polypeptide. The invention further comprises an isolated nucleic additionable properties. The invention further comprises an isolated nucleic additionable by the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide has the following activities; antilipaemic, cardiant, vasotropic, antiatrerioscolerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

The invention relates to a novel synthetic apolipoprotein-E mimicking

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antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (LDL) to a cell and enhances degradation of LDL or mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease, dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant;
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                                                                                                                                                                                                      Score 94; DB 8; Length 10, Pred. No. 2.6e-07;
                                                                                                                                                                                                                                                     2; Mismatches
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                                                                                                                                                                                                                      95.9%;
88.9%;
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                                                                                                                                                                                                                                                                                                  1 GIRRFIGSIWRFLRAFYG
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Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                          Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                          AD034339;
                                                                                                                                                                                                                                                                                                                                                             RESULT 11
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us-10-712-447-10.rag

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useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein. E mimicking polypeptide enhances binding of low-density lipoprotein (ULD) to a cell and enhances degradation of tub. or VLDL by a cell. This sequence represents a synthetic apolipoprotein. E mimicking mimicking polypeptide of the invention.
                  88888888888888888
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Sequence 18 AA;

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                        Gaps
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0
 Length 18;
  Score 94; DB 8; I
Pred. No. 2.6e-07;
                        Mismatches
                         2;
                                                1 GIRRFLGSIWRFIRAFYG 18
                                                                       1 GLRRFIGSIWRFIRAFYG 18
  95.9%;
Query Match
Best Local Similarity 88.9 Matches 16; Conservative
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Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 74.
     ADO34297 standard; peptide; 18 AA
                12-AUG-2004 (first entry)
          ADO34297;
RESULT 12
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apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbeterlipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; ULDL.

Synthetic

402004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

ö Datta Garber DW, Anantharamiah GM,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 74; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide and activities: antilipaemic, cardiant, vasotropic, antiarteriosolerotic, cerebroprotective, and antiandinal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal

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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-B mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and acrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and cartical antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
                                                                                                                                                                                                                                                                                          ò
             chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of mycozrdial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
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such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant;
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                                                                                                                                                                                                                                              Score 92; DB 8; Length 18;
Pred. No. 5.3e-07;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO34244 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                Query Match 93.9%;
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                           1 GIRRFLGSIWRFIRAFYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UABR-) UAB RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anantharamiah GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MO2004043403-A2.
                                                                                                                                                                                                             Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADO34244;
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO34244
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chimpanzee or orangutan); for treating coronary artery disease, despetablishments or atherospecierosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking oblypeptiale enhances binding of low-density lipoprotein (IDL) or very low density lipoprotein (VLDL) to a cell, and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
                                                                                                                                                                                                                                                                                                                                                                                                                                     apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "All Lys residues are DiMethyl-Lysine"
                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 53.
                                                                                                                                                             DB 8; Length 18;
                                                                                                                                                                                        Indels
                                                                                                                                                           93.9%; Score 92; DB 8; Le:
88.9%; Pred. No. 5.3e-07;
ive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Datta G;
                                                                                                   mimicking polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                 18
                                                                                                                                                                                                                                                                                                                        ADO34276 standard; peptide; 18
                                                                                                                                                                                                                     1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anantharamiah GM, Garber DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-NOV-2003; 2003WO-US036268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-2002; 2002US-0425821P.
                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                         Local Similarity 88.9
es 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UABR-) UAB RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-411629/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004043403-A2
                                                                                                                                Sequence 18 AA;
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                12-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                   AD034276;
                                                                                                                                                             Query Match
                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                         ADO34276
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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

Claim 4; SEQ ID NO 53; 79pp; English

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antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or oranguten); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or wimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypudleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and apolipoprotein-E mimicking polypeptide and a carrier; and aminicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiatreriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasctropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholestron; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL;
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic apolipoprotein-E mimicking related R18L linear peptide.
                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                Score 92; DB 8; Length 18;
Pred. No. 5.3e-07;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO34227 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                      1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garber DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-NOV-2003; 2003WO-US036268.
                                                                                                                                                                                                                                                                                                     93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-NOV-2002; 2002US-0425821P
                                                                                                                                                                                                                                                                                                                                                                                                              1 GIKRFLGSIWRFIKAFYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                            16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-411629/38.
                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                             Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004043403-A2
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                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
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useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, dyshetalipoproteinneemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein. E mimicking apolypeptide enhances binding of low-density lipoprotein (ULD) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein.
               888888888888888
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Sequence 18 AA;

ö 0; Gaps Query Match
91.8%; Score 90; DB 8; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 1; Indels

Search completed: May 19, 2006, 14:24:31 Job time: 94.2857 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

May 19, 2006, 14:24:57; Search time 14.2857 Seconds (without alignments) 121.233 Million cell updates/sec Run on:

US-10-712-447-10 98 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 GIRRFLGSIWRFIRAFYG 18 Scoring table: Sequence:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

lesult		* Query				-
No.	Score	Match	Match Length	8	ID	Description
-	48	49.0	627	7	S76462	hypothetical prote
7	45	45.9	178	~	A75578	transcription regu
e	44	44.9	461	٦	G64537	2-oxoglutarate/mal
4	44	44.9	589	7	A34341	poly (3-hydroxybuty
'n	44	•	806	~	A84060	leucyl-tRNA synthe
9	44	44.9	861	~	H64102	leucine-tRNA ligas
7	43.5	44.4	1025		AH3568	acriflavin resista
ω	4	43.9	265		T32316	hypothetical prote
6	43	43.9	489		B84733	probable cytochrom
10	43	43.9	516		T33269	hypothetical prote
11	43	43.9	812		A46417	NIP1 protein - yea
12	43	43.9	1607		T04583	TMV resistance pro
13	42.5	43.4	407		T12085	reverse transcript
14	42.5	43.4	760	•	E84953	penicillin-binding
15	42	42.9	107	•	T52113	G
16	42	42.9	214		D72540	hypothetical prote
17	42	42.9	228		T15530	hypothetical prote
18	42	42.9	237		B72692	hypothetical prote
19	42	42.9	246	~	154412	MHC HLA-A cell sur
50	42	42.9	258		F71707	
21	42	42.9	258		D97700	o-antigen export B
22	42	42.9	273		нгниев	
23	42	42.9	365		HLHUA2	MHC class I histoc
24	42	42.9	365		I38443	HLA-A-0
25	42	42.9	365		I61902	class I
26	42	42.9	365		137542	class I
27	42	42.9	365		I84448	
28	42	42.9	365		161857	ILA-A2.4a ch
29	42	42.9	365		138442	gene HLA-A-0205 pr

hypothetical prote leucyl-tRNA synthe leucyl-tRNA synthe	leucyl-rRNA Bynthe leucine-tRNA ligas homolog to drosoph	nypothetical prote rfaP protein - Esc dimethylsulfoxide hypothetical prote	hypothetical prote probable permease hypothetical prote	hypothetical prote hypothetical prote cytochrome P450 DW
T04745 AD1282 AH1653	B89961 D69650 T50337	AG2115 C42595 E64109 T20575	AF2599 G97381 T08940	F96571 D96776 T02263
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537 803 803	804 804 790	131 265 279 359	364 364 384	406 503 519
4 4 4 2 2 . 9 9 . 9 9 . 9 9 . 9		4 4 4 4 1 1 1 4 8 8 8 8		
4 4 4 2 2 2 2	42 42 41.5	4 4 4 4 1 1 1 1 1	444	4 4 4
30 31 32	. W W W .	9 W W W W	0444 0112	4 4 4 6 4 0

## ALIGNMENTS

;	RESULT 1 Synechocystis sp. (strain PCC 6803) C;Species: Synechocystis sp. (strain PCC 6803) C;Species: Synechocystis sp. A;Variety: PCC 6803 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004 C;Accession: S76462 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 31, 109-136, 1996 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
	A,Reference number: S74322; MUID:97061201; PMID:8905231 A,Accession: S76462 A,Status: prealiminary A,Status: prealiminary A,Festuary Prealiminary A,Festuary Parellminary A,Festuary Parellminary A,Festuary DAA A,Residues: 1-627 <kan> A,Festuary DAA A,Residues: 1-627 <kan> A,Festuary DAA A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 Query Match Best Local Similarity 38.9%; Pred. No. 8.1; Best Local Similarity 38.9%; Pred. No. 8.1; Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;</kan></kan>

1 GIRRFLGSIWRFIRAFYG 18 ઠે

|::||||::| 597 GLEQLLGKIWQWLRQKFG 614 qq

Lranscription regulator, Mark family - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004
C;Date: 03-Dec-1599 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004
C;Date: 03-Esson, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F;White, Shen, M.; Vamathevan, J.G.; Fraser, C.M.
S.; Smith, H.O.; Venter, J.G.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: A75578 A;Status: preliminary A;Molecule type: DNA

A;Residues: 1-178 <WHI>
A;Cross-references: UNIPROT:Q9RYRO; UNIPARC:UPI00000D3BE4; GB:AE001863; GB:AE001825; NID:
A;Experimental source: strain R1
C;Genetics:
A;Cene: DRA0248
A;Map position: 2

Query Match

45.9%; Score 45; DB 2; Length 178;

N

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Authors: Gnehm, R.C.; Moronald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, G. A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, U.D.; Scott, U.J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, U.D.; Scott, U.J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, U.D.; Scott, U.J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, U.D.; Scott, U.J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, U.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, U.L.; Fuhrmann, U.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C. A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: Ad4000; MUID:95350630; PMID:7542800
A;Accession: H64102
A;Status: nucleic acid sequence not shown; translation not shown
A;Residues: 1-861 <TICR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cispecies: Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession, AH3568
F;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc
                                                                                                                                                                                                                                             CjAccession: A84060
R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and characterence number: A83650; MUID:20512582; PMID:11058132
A; Accession: A84060
A; Status: preliminary
A; Status: preliminary
A; Residues: 1-806 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Cross-references: UNIPROT.09K7S8; UNIPARC:UPI0000136555; GB:AP001518; GB:BA000004; NID:
A.Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                leucyl-tRNA synthetase leuS [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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C;Superfamily: leucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 2; Length 861;
Pred. No. 48;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.9%; Score 44; DB 2; 53.8%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
100 RRFAGDAWRINLPYRFAAAFY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Genetics:
A,Gene: leuS
C,Superfamily: leucine-tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.9%;
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622 GARRFLDRVWRLL 634
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Best Local Similarity 46.4.
Best Local 6; Conservative
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Matches 7; Conservative
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R;Tomb J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
R;Tomb J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kellay, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cispecies: Alcaligenes eutrophus
Cispecies: Alcaligenes eutrophus
Cispecies: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
Ciscession: A34341; A39190
Rispeoples, O.P.; Sinskey, A.J.
Cispecies, O.P.; Sinskey, A.J.
Chen: 264, 15298-15303, 1989
A;Title: Poly-beta-lydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Iden
A;Reference number: A34341; MUID:89359357; PMID:2670936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.Schubert, P.; Krueger, N.; Steinbuechel, A.
J. Bacteriol. 173, 168-175, 1991
A;Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynt
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A;Residues: 1-219 <SCH>
A;Cross-references: UNIPARC:UPIO00016E162; GB:M64341; NID:g141964; PIDN:AAA21979.1; PID:
A;Note: the authors translated the codon TAC for residue 120 as Thr
C;Superfamily: poly(3+hydroxyalkanoic acid) synthase phbC
C;Keywords: acyltransferase
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A;Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:g141958; PIDN
A;Experimental source: strain H16
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                Gaps
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Pred. No. 26;
2; Mismatches 4; Indels
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                                Indels
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69.2%;
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                                                                                            2 IRRFLGSIWRFIR 14
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Best Local Similarity 69.2
Matches 9; Conservative
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Best Local Similarity 53.8
Matches 7; Conservative
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A; Residues: 1-461 <TOM>
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A, Status: preliminary
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A; Status: preliminary
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Nipi protein - yeast (Saccharomyces cerevisiae)
NiAlternate names: nuclear import protein; protein YM9924.01c; protein YM9952.11c; protei)
C;Species: Saccharomyces cerevisiae
C;Spacession: A46417; SS3979; SS39302
R;Gu, Z.; Moerschell, R.P.; Sherman, F.; Goldfarb, D.S.
Proc. Natl. Acad. Sci. U.S.A. 89, 10355-10359, 1992
A;Tille: NIPI, a gene required for nuclear transport in yeast.
A;Reference number: A46417; MUID:93066237; PMID:1332047
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A;Cross-references: UNIPARC:UPI000168ACA; EMBL:Z54141; NID:g1072408; PID:g984682; MIPS:)
A;Experimental source: strain AB972
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A;Residues: 571-582,'Q',584-640,'K',642,'K',644-812 <CON>
A;Cross-references: UNIPARC:UP10000168ACD; EMBL:Z49212; NID:g798940; PID:g798951; MIPS:YN
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                                     P450 homology
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33269
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A; Residues: 1-812 <GU1>
A; Residues: 1-812 <GU1>
A; Residues: UNIPROT: P32497; UNIPARC: UDI000017B2B1; EMBL: L02899
A; Note: sequence extracted from NCBI backbone (NCBIN:117849, NCBIP:117850)
R; Connor, R.; Churcher, C.M.
Bubmitted to the EMBL Data Library, April 1995
A; Reference number: S53969
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A;Map position: 2 C;Superfamily: Synechocystis cytochrome C;Superfamily: Synechocystis cytochrome
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A;Description: The sequence of C. elegans cosmid C24B9
A;Reference number: Z21310
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A,Molecule type: DNA
A,Residues: 1-516 <MUR>
                                                                                                        Score 43; DB 2;
Pred. No. 40;
4; Mismatches
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43.9%; Score 43; DB 2;
Best Local Similarity 41.2%; Pred. No. 42;
Matches 7; Conservative 5; Mismatches
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submitted to the EMBL Data Library, September 1995
A;Reference number: 559302
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A;Map position: 5
A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2
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54.5%;
                                                                                                               Query Match
Best Local Similarity 54.5
Matches 6; Conservative
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54 IGNMWSFLRAF
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A;Molecule type: DNA
A;Residues: 1-1025 <KUR>
A;Cross-references: UNIPROT:Q8YCQ5; UNIPARC:UPI00000584C8; GB:AE008918; PIDN:AAL53715.1;
A;Experimental source: strain 16M
       Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
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A;Experimental source: strain Bristol N2; clone F31F4
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AjMOLecule type: DNA
Kresidues: 1-489 «STO»
Ajcross-references: UNIPROT:Q9ZV72; UNIPARC:UPI000009D8ED; GB:AE002093; NID:G3831452;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb.2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F31F4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
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A;Introns: 13/3; 67/2
C;Superfamily: Caenorhabditis elegans hypothetical protein T09F5.1
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Pred. No. 69;
4; Mismatches
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Pred. No. 22;
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C,Superfamily: hypothetical protein b2075
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531 FLGSVWSFMTLPRSFF 546
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ilarity 53.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 FLGSIWRFI --- RAFY 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.09
Matches 8; Conservative
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: CESP: F31F4.4
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                                                                                                                                  A; Accession: AH3568
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                                                                                                                                                                                                                                                                                                                                                                         A;Gene: BMEII0473
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Score 43; DB; Pred. No. 66; 4; Mismatches

Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative

|::| ||||: |: 361 GVKRILGSIFSFV 373 1 GIRRFLGSIWRFI 13

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RESULT 12

A;Gene: SGD:NIP1 A;Cross-references: SGD:S0004926; MIPS:YMR309c A;Map position: 13R

C; Genetics:

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probable transcription co-activator KIWI [imported] - Arabidopsis thaliana cispecies: Arabidopsis thaliana (mouse-ear cress)
c; Species: Arabidopsis thaliana (mouse-ear cress)
c; Date: 20-oct-2000 #sequence_revision 20-oct-2000 #text_change 09-Jul-2004
C; Accession: T52113
R; Cormack, K.S.; Hahlbrock, K.; Somssich, I.E.
Plant J. 14, 685-92, 1998
A; Title: Isolation of putative plant transcriptional coactivators using a modified two-hy A; Reference number: Z25848; MUID:98346011; PMID:9681033
A; Accession: T52113
A; Accession: T52113
A; Accession: T52113
A; Molecule type: mRNA
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A;Residues: 1-107 <COR>
A;Residues: 1-107 <COR>
A;Residues: 1-107 <COR>
A;Cross-references: UNIPROT:O65154; UNIPARC:UPI000000C45F; EMBL:AF053302; PIDN:AAC08574.3

A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: KIWI
A;Amap position: V
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C;Superfamily: Caenorhabditis elegans hypothetical protein T13F2.2
                                                                                                                                                                                                                                                                                                                      Nature 407, 81-86, 2000
A,Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
A,Reference number: A84930; MUID:20445173; PMID:10993077
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                                                                                                                                                                                                 C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Accession: E84953
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                                                                                                                                                                                                                                                                                                                                                                                                                                A, Residues: 1-760 <STO>
A, Residues: 1-760 <STO>
A, Cross-references: UNIPARC: UPI000005E4C8; GB: AP000398; GSPDB:GN00144
A, Experimental source: strain APS
C, Genetics:
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                                                                                                                                                                     penicillin-binding protein 1b [imported] - Buchnera sp. (strain APS)
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                                                                                                                                                                                                                                                                               R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa,
Nature 407, 81-86, 2000
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13;
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Pred. No.
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178 GIRSFLGHVGFYRRFIRDF 196
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Best Local Similarity 50.0%;
Matches 8; Conservative
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Matches 8; Conservative
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A, Gene: mrcB; BU200
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A;Molecule type: DNA
A;Residues: 1-1607 -8BEV>
A;Cross-references: UNIPROT: O65506; UNIPARC: UPI00000AA45C; EMBL: AL022141
A;Cross-references: UNIPROT: Columbia; BAC clone F23E13
A;Experimental source: cultivar Columbia; BAC clone F23E13
R;Bevan, M.; Wedler, H.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schuelle submitted to the Protein Sequence Database, April 1998
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A;Molecule type: mRNA
A;Residues: 1-407 <KINN>
A;Cross-references: UNIPROT: 022103; UNIPARC: UPI00000AAD3D; EMBL: AB007466; NID: d1170509;
A;Experimental source: guard cell protoplasts
C;Superfamily: pol polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TMV resistance protein N homolog F23E13.30 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C;Accession: T04583; T05507 M.; H05807 M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse, submitted to the Protein Sequence Database, March 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: T12085
R;Kinoshita, T.; Wada, H.; Masaaki, I.; Shimazaki, K.
submitted to the EMBL Data Library, September 1997
A,Description: Retrotransposon-like cDNAs from guard cell protoplasts in Vicia faba.
A,Reference number: Z17406
A;Reference number: Z17406
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C,Species: Vicia faba (fava bean)
C,Date: 16-Jul_1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
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Pred. No. 1.3e+02;
0; Mismatches 3; Indels
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A;Cross-references: UNIPARC:UP1000016DBFD; EMBL:AL022373 A;Experimental source: cultivar Columbia; BAC clone T19K4

A; Residues: 1448-1607 <BE2>

A; Molecule type: DNA

A; Reference number: Z15418

A;Map position: 4 A;Introns: 193/2; 238/2; 556/2; 930/3; 1029/3; 1287/3 A;Note: F23E13.30; T19K4.270

43.9%; ilarity 72.7%; Conservative

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Gaps

3,

4; Indels

13.4%; Score 42.5; Dilarity 57.9%; Pred. No. 40; Conservative 1; Mismatches

Query Match Best Local Similarity Matches 11; Conserva

1 GIRRFLGSIW---RFIRAF 16

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DB 2; Length 407;

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Q25271_LEPDE
Q957V7_RH1LV
Q44QD1_CHLLI
Q43KQ1_9CHLB
Q39L57_BURK3
Q456F4_9BURK
XKR7_PANTR
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XKR7_PANTR
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039K79 PARDE
084ZW1 PEA
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P74489 SYNY3

P97035 HAESO

036K84 RHOPA

036K84 RHOPA

037C12 RHOPA

037C12 RHOPA

031K9 SENLA

65UH14 KENLA

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65UH14 KENLA

65UH16 SENLA

65UH1
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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brachydanio rattus norv homo sapien colorobium nitrosospir magnetococc salinibacte cryptospori deinococcus picrophilus burkholderi bordetella bordetella	Glavina T., arimer F.,	Gaps
Q5gh40 Q5gh57 Q5gh57 Q5kh73 Q2y8v4 Q2xw00 Q3xw00 Q5cpz7 Q5cpz7 Q6b115 Q4b115 Q7vv93 Q7vv93	m 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	IGA.  IEA.  igase.  igase.  indels 0  i Indels 0  i Pterygota;  ita, Pterygota;  ita, Pterygota;
n 7545404040	ALIGNMENTS  T.  S. CHLCH  GJAPYS.  22-NOV-2005, integrated into UniProtKB/TrEMBL.  22-NOV-2005, sequence version 1.  21-EBB-2006, entry version 5.  Leucyl-tRNA synthetase class Ia (EC 6.1.1.4).  OrderedicousNames—cag_168;  Chlorobium Chlorochromatii (Brain CaD3).  Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiance, Chlorobium/Pelodictyon group; Chlorobium.  NUCLEDTID SEQUENCE [LARGE SCALE GENOMIC DNA].  US DOE Joint Genome Institute;  Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C.  Hammon N., Israni S., Pitluck S., Bryant D., Schmutz J.,  Land M., Kyrpides N., Ivanova N., Richardson P.;  "Complete sequence of Chlorobium chlorochromatii CaD3.";  Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.  Copyrighted by the UniProt Consortium, see http://www.un.	Distributed under the Creative Commons Attribution-Noberlys in the Creative Commons Attribution-Noberlys in the Creative Commons Attribution-Noberlys in the Creative Complete Series of GO:0004524; F.ATP binding; IEA.  GO:0016874; F.Higase activity; IEA.  Aninoacyl-tRNA synthetase; Complete proteome; Ligase.  SEQUENCE 805 AA; 92007 MW; A0C78B83732AF54C CRC64;  T.Y.  GO:0016874; F.HIGASTARFI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Q5GH40 BRARE XKR6 RAT XKR6 HUMAN XKR6 HUMAN SYL, CHLTE Q2YBV4 NITMU Q3XW00 9PROT Q25415 9SPHI Q25PZ7 CRYPV Q5CPZ7 CRYPV Q5CPZ7 CRYPV Q4CNS1 BURVI Q7WV93 BORPE Q7WY7P3 BORPE	NULT 1  OJARYS CHLCH OJARYS CHLCH PRELIMINARY; PRT; 805 AA. OJARYS CHLCH PRELIMINARY; PRT; 805 AA. DANOW-2005, integrated into UniProtKB/TrEMBL 22-NOW-2005, sequence version 1. 22-NOW-2006, entry version 5. Leucyl-tRNA synthetase class Ia (BC 6.1.1.4). Orderediocundames-cag_1688; Chlorobium chlorochromatii (strain CaD3). Bacteria, Chlorobi; Chlorobia; Chlorobiales; Chlorobium/Pelodictyon group; Chlorobiales; (MSI_TAXID=340177; 11] WUCELTAXID=340177; Copeland A., Lucas S., Lapidus A., Barry K., Hammon N., Isarai S., Pitluck S., Barry K., Land M., Kyrpides N., Pitluck S., Barry K., Land M., Kyrpides N., Pitluck S., Barry K., Land M., Kyrpides N., Pitluck S., Richardson "Complete sequence of Chlorobium chlorochroma Submitted (ANG-2005) to the EMBL/GDBJAK/DDBJ COPYTIGHTED SEQUENCE CONSOTTIUM, see Pit	nder the Creative Commons Attriby ABB28940.1; -; Genomic_DNA. 4; F:ATP binding; IEA. 4; F:14gase activit; 3; F:14gase activit; 4; F:15gase activit; 1EA. 5; P:1eucyl-tRNA aminoacylation; A synthetase; Complete proteome; 5 AA; 92007 WW; AC78B83732AF5; 5A; 9207 WW; AC78B83732AF5; COMPLIAN COMPLET
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preliminary data.
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STRAIN=DSM 245;
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Q44QD1;
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016687; F:ATPase activity; IEA.
GO; GO:0014626; F:ATPase activity; coupled to transmembrane m. . .; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0008565; F:protein transporter activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                        de Kort C.A.D., Koopmanschap A.B.; "Nucleotide and deduced amino acid sequence of a cDNA clone encoding diapause protein 1, an amylphorin-type storage hexamer of the Colorado
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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"Analysis of the genetic region encoding a novel rhizobiocin from
Rhizobium leguminosarum bv. viciae strain 305.";
Can. J. Microbiol. 47:495-502(2001).
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Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                          55.1%; Score 54; DB 2; Length 670; 43.8%; Pred. No. 11; ive 6; Mismatches 3; Indels
Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;
                                                                                                                                                                                                                                                                                                                                     670 AA; 79825 MW; 8A000BA115BEC8A6 CRC64;
                                                                                                                                                                                       GO; GO:0005344; F:oxygen transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000896; Hemcoyanin.
InterPro; IPR005203; hemcoyanin.
InterPro; IPR005204; hemcoyanin.
PANTHER; PTHR11511; Hemcoyanin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2001, integrated into UniProtKB/TrEMBL 01-WAR-2001, sequence version 1. 07-FEB-2006, entry version 25. ABC transporter RzcB.
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                                                                                                                                                                                                                                                                                              PRINTS; PRO0187; HAEMOCYANIN.
PROSITE; PS00210; HEMOCYANIN_2; UNKNOWN_1.
NON TER
SEQUENCE 670 AA; 79825 MW; 8A000BA115B
                                                                                                      J. Insect Physiol. 40:527-535(1994)
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                                                                                                                                                                 EMBL; X76080; CAA53691.1; -; mRNA.
                                                                                                                                                                                                                                                               Pfam, PF03723; Hemocyanin_C; 1.
Pfam, PF00372; Hemocyanin_M; 1.
Pfam, PF03722; Hemocyanin_N; 1.
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351 RKFYGALWSYLRHFFG 366
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                                              NUCLEOTIDE SEQUENCE
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Matches 7; Conserv
             Leptinotarsa.
NCBI_TaxID=7539;
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Q9F7V7 RHILV
Q9F7V7;
                                                                                               potato beetle."
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Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
Sequencing of the draft genome and assembly of Chlorobium limicola
DSM 245.";
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Larimer F., Land M.;
"Annotation of the draft genome assembly of Chlorobium limicola DSM
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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13-SEP-2005, sequence version 1.
14-SEP-2006, entry version 3.
16-UFB-2006, entry version 9.
16-UFB-1-RNA synthetase bacterial/mitochondrial, class Ia.
16-UCyl-1-RNA synthetase bacterial/mitochondrial, class Ia.
16-UCyl-1-RNA synthetase bacterial/mitochondrial, class Ia.
18-UCYL-1-RNA synthetase bacterial/mitochondrial, class Ia.
18-UCYL-1-RNA synthetase bacterial/mitochondrial, class Ia.
18-UCYL-1-RNA synthetase bacterial/mitochondrials
18-UCYL
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004823; F:Leucine-tRNA ligase activity; IEA.
GO; GO:00429; P:Leucyl-tRNA aminoacylation; IEA.
InterPro; IPR002332; Leu tRNAsyn_la.
Pfam; PF00133; tRNA-synt_l; 1.
GO; GO:0015031; P:protein transport; IEA.
GO; GO:0006508; P:proteolysis; IEA.
InterPro; IPR01527; ABC_TM 1.
InterPro; IPR011527; ABC_TM 1.
InterPro; IPR01140; ABC_TM 1.
InterPro; IPR03439; ABC_Transpt.
InterPro; IPR05074; Peptidase C39.
InterPro; IPR0112; Type I sec HlyB.
PANTHER; PTHR1924: SFT4; Type I sec HlyB.
PANTHER; PF00064; ABC_membrane; I.
Pfam; PF00065; ABC_tran; 1.
Pfam; PF00005; ABC_tran; 1.
Propon; PD000006; ABC_transporter; 1.
PROSITE; PS0021; AAA; I.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
PROSITE; PS00990; PSPFIDABE, C39; 1.
PROSITE; PS0990; PSPFIDABE, C39; 1.
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RESULT 5

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                                                           22-NOV-2005, sequence version 1.
21-FEB-2006, entry version 4.
Hypothetical protein.
OrderedLocusNames=Beep18194 A3207;
Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760 / NCIB 9086 / R18194)).
                                                                                                                                                                                                                                                                                                 US DOE Joint Genome Institute;
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M., Hammon N., Israni S., Larimer F., Land M., Kyrpides N., Lykidis A., Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Larimer F., Land M.; "Annotation of Burkholderia cenocepacia" Annotation of the draft genome assembly of Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burkholderia cenocepacia AU 1054.
Bacteria; Proteobacteria; Betaproteobadteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                                                                                                                                                       Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                                                                                                                                                                                                                                                                                                                                                                  "Complete sequence of chromosome 1 of Burkholderia sp. 383.";
Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.0%; Score 51; DB 2; Length 407; 47.1%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; CP000151; ABB06809.1; -; Genomic_DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;
                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-SEP-2005, integrated into UniProtKB/TrEMBL. 13-SEP-2005, sequence version 1. 07-FEB-2006, entry version 2. Hypothetical protein.
  039157 BURS3 PRELIMINARY; PRT; 407 AA. 039157; 22-NOV-2005, integrated into UniProtKB/TrEMBL
407 AA.
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US DOE Joint Genome Institute (JGI-ORNL);
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Q456F4;
PRT;
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327 GIRQMLGHVWQWTRSSY 343
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nes 8; Conservative
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Chlorobium phaeobacteroidde DSM 266.
Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
Chlorobium/Pelodictyon group; Chlorobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Chlorobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.1%; Score 52; DB 2; Length 816; 61.5%; Pred. No. 29; ive 2; Mismatches 3; Indels
                                                                                                          Length 805;
                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2006, entry version 9.
Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phaeobacteroides DSM 266.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=DSM 266;
US DOB Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Chlorobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               816 AA; 93335 MW; 6770B1DAC50560F1 CRC64;
                        TIGREAMS; TIGR00396; leus_bact; 1.
Aminoacyl-tRNA synthetase.
SEQUENCE 805 AA; 91997 MW; D4F3FE28F9E92DF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AAIB01000002; EAM35935.1; -; Genomic_DNA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:00048323; F:leucine-tRNA ligase activity; IEA.
GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
                                                                                                       Score 52; DB 2;
Pred. No. 29;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2005, integrated into UniProtKB/TrEMBL. 13-SEP-2005, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                816 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro: JPR002302; Leu TRNAsyn_la.
Pfam, PF00133; TRNA-synt_1; 1.
PRINTS; PR00985; TRNASYNTHLEU.
TIGREAMS; TIGR00396; leus_bact; 1.
Aminoacyl-tRNA synthetase.
SEQUENCE 816 AA; 93335 MW; 677081
                                                                                                                                                                                                                                                                                                                                                PRT;
        PRINTS; PR00985; TRNASYNTHLEU
                                                                                                              53.1%;
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GISRFLGKVWRLV 634
                                                                                                                                                                                                                                          622 GISRFLGKVWRLV 634
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                                                                                                                                                                                              1 GIRRFLGSIWRFI 13
                                                                                                          Query Match
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phaeobacteroides DSM 266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=290317;
                                                                                                                                                                                                                                                                                                                                                Q43K01_9CHLB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=DSM 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         622
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Q39L57_BURS3
                                                                                                                                                                                                                                                                                                                              9CHLB
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Matches

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Gaps

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4; Indels

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WELECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

WUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

WEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

Deloukas P., Mathews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,

Deloukas P., Mathews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,

And Jones M., Stavrides G., Almeida J.P., Beard L.M., Beare D.M.,

Basiley O.E., Bird C.P., Blakey S.E., Briddeman A.M., Brown A.J.,

Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

Chapman J.C., Clamp M., Clark E.N., Clark S.Y., Clee C.M.,

Clegg S., Cobley V.E., Collier R.E., Cohnor R.E., Corby N.R.,

Clegg S., Cobley V.E., Collier R.E., Cohnor R.E., Dunn M.,

Clegg S., Cobley V.E., Collier R.E., Cohnor R.E., Dunn M.,

Clegg S., Farahland J.A., Fraeer A., French L., Garner P.,

Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

Hunckle E., Hunt A.R., Hutt S.E., Jekosch K., Johnson D.,

RAY M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

Mills S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

A knice C.M., Ross M.T., Scott C.E., Schra H.K., Shownkeen R., Sims S.,

Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,

Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,

Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,

Mitchead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Whitchead S.L., Whittaker P., Willey D.L., Williams E.,

Whitchead S.L., Whittaker P., Willey D.L., Williams E.,

Whitchead S.L., Whittaker P., Willey D.L., William S.N.,

Whitchead S.L., Whittaker P., Willey D.L., William S.N.,

Whitchead S.L., Whittaker P., Willey D.L., William S.N.,

Whitchead S.L., Whittaker P., Willey D.L., William S.D.K.,

Whitchead S.L., Whittaker P., Willey D.K., Wallis, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential).
--- SMILARITY: Belongs to the XK familý.
--- CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 414:865-871(2001).
-!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.0%; Score 50; DB 1; Length 579; 58.3%; Pred. No. 42; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                   Huang C.-H., Chen Y.; "A superfamily of XK-related genes (XRG) widely expressed
                                                                                                                                                                                                                                                                                                                 vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D8D0FF64B9EDD53D CRC64;
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EMBL; AL031658; CAB88102.1; ALT_SEQ; Genomic_DNA.
Ensembl; ENSG0000101321; Homo saplens.
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Name=XKR7; Synonyms=C20orf159, XRG7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63826 MW;
                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [MRNA].
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355
384
415
579 AA;
                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US DOE Joint Genome Institute (JGI-BGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Larimer F., Land M., "Annotation of the draft genome assembly of Burkholderia cenocepacia
         Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                          ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burkholderia cenocepacia H12424.
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, Burkholderia, Burkholderia cepacia complex.
                                                                                                                                                                                     52.0%; Score 51; DB 2; Length 408; 47.1%; Pred. No. 20; 47.1% arive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.0%; Score 51; DB 2; Length 408; 47.1%; Pred. No. 20; tive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HI2424.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                 Hypothetical protein.
SEQUENCE 408 Aa, 45545 MW; 3C2BCA9471BAAE93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 408 AA; 45603 MW; 7F393888305911D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XKR7 HUMAN STANDARD; PRT; 579 AA. Q5GH72; Q9NUG5; 11-OCT-2005, integrated into UniProtKB/Swiss-Prot. O1-MAR-2005, sequence version 1. O7-FRB-2006, entry version 8. XK-related protein 7.
                                                                EMBL; AAHI01000010; EAM12352.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AAHL01000063; EAM16412.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-AUG-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       408 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=H12424;
US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-2005, sequence version 1.
07-FEB-2006, entry version 2.
Hypothetical protein.
ORFNames=Bcen2424DRAFT_1071;
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GIROMLGHVWOWTRSSY 344
                                                                                                                                                                                                                                                                                                                                                           328 GIRQMLGHVWQWTRSSY 344
                                                                                                                                                                                                                                                                                                                       1 GIRRFLGSIWRFIRAFY 17
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                                                                                                                                                                                                                      Local Similarity 47.1 les 8; Conservative
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Q4LK44;
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                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                               11-0CT-2005, integrated into UniProtKB/Swiss-Prot.
13-SEP-2005, sequence version 1.
13-SEP-2005, sequence version 6.
13-SEP-2006, entry version 6.
XK-related protein 7.
Name=XKR7; Synonyms=XRG7;
Pan troglodytes (Chinganzee).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                             Huang C.-H., Chen Y.;
"A superfamily of XK-related genes (XRG) widely expressed in vertebrates and invertebrates.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 579;
                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                    6DFE1191093E85D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                  XK-related protein 7./FTId=PRO_0000190790.Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          580 AA
                  579 AA.
                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 42;
                                                                                                                                                                                            (Potential).
                                                                                                                                                                                                                                                                                                                                                                       Score 50;
                                                                                                                                                                                                                                                                                                                  Potential
                                                                                                                                                                                                                                                                                               Potential
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                                                                                                                                                                                                                                                                                                                                   Potentia
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                                                                                                                                                                                                                                                  EMBL; AY702910; AAV83783.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2005, sequence version 1.
07-FEB-2006, entry version 10.
XK-related protein 7.
                                                                                                                                                                                                                                                                                                                                                     63593 MW;
                                                                                                                                                                                                                                                                                                                                                                       51.0%;
                                                                                                                                    NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Xkr7; Synonyms=Xrg7;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                       || :||::|| |
190 LGQVWRYLRALY 201
                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          6 LGSIWRFIRAFY 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                  STANDARD;
                                                                                                                                                                                                                                                            Membrane; Transmembrane
                                                                                                                                                                                                                                                                                                                                              415 4
579 AA;
                                                                                                                     NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XKR7 MOUSE
                  PANTR
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q5GH64;
                         049131;
RESULT 10
XKR7_PANTR
ID XKR7 P.
                                                                                                                                                                                                                                                                     CHAIN
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                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegius (Rat).
Eukaryota; Metazoa (Rat).
Mammalia; Butheria; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huang C.H., Chen Y.,
"A superfamily of XK-related genes (XRG) widely expressed in
"A superfamily of XK-related in vertebrates ";
"A superfamily of XK-related ";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-:- SUBCELLUMAR LOCATION: Membrane; multi-pass membrane protein
-!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                Score 50; DB 1; Length 580;
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                              2; Indels
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                                                                                                                                                                                                                                                                            Potential.
F3291FABF4C5A826 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XK-related protein 7.
/FTId=PRO_0000190791.
Potential.
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2005, integrated into UniProtKB/SwiBB-Prot.
                                                                                                                                                    /FTId=PRO_0000190789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         580 AA
                                                                                                                                                                                                                                                                                                                                              3, Mismatches
                                                                                          EMBL; AY534253; AAT07102.1; -; mRNA.
Ensembl; ENSMUSG00000042631; Mus musculus.
MGI; MGI:3526711; Xkr7.
Membrane; Transmembrane.
                           -!- SIMILARITY: Belongs to the XK family.
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Potential.
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Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2005, sequence version 1.
OY-FBB-2006, entry version 8.
XK-related protein 7.
Name-Xkr7; Synonyms=Xrg7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64338 MW;
                                                                                                                                                                                                                                                                                         64302 MW;
                                                                                                                                                                                                                                                                                                                   51.0%;
58.3%;
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STRAIN=Sprague-Dawley;
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190 LGOVWRYLRALY 201
                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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109
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323
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580 AA;
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               (Potential).
                                                                                                                                                                                                                      303
326
355
384
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326
355
384
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Best Local S
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Q5GH56;
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TRANSMEM
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                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                 Matches
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07-FEB-2006, entry version 4.
                                                                                                                                                                                                                                                                                                              STRAIN=PD1222
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Q842W1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=KA01
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   DDD BRAND BR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Larimer F., Land M.; "Annotation of the draft genome assembly of Burkholderia vietnamiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US DOE Joint Genome Institute (JGI-PGF);

Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;

Submitted (JUN-2005) to the BMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burkholderia vietnamiensis G4.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.0%; Score 49; DB 2; Length 409; Best Local Similarity 41.2%; Pred. No. 42; Matches 7; Conservative 5; Mismatches 5; Indels
                            Score 50; DB 1; Length 580; Pred. No. 42;
                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 409 AA; 45629 MW; CCD3FA52A9F014E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AAEH02000029; EAM28562.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OJEKTO PARDE PRELIMINARY; PRT; 449 AA.

1D OJEKTO PARDE PRELIMINARY; PRT; 449 AA.

2 PARTO PARTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                      409 AA.
                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2005, sequence version 1.
07-FEB-2006, entry version 2.
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                                51.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry version 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORFNames=Bcep1808DRAFT_3388;
                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
   Query Match
Best Local Similarity 58..
7; Conservative
                                                                                                                                                                                                                                         190 LGOVWRYLRALY 201
                                                                                                                                                                         6 LGSIWRFIRAFY 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary data.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=269482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vietnamiensis G4
                                                                                                                                                                                                                                                                                                                                                                                                                  Q4BFM2_BURVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Larimer F., Land M.; "Annotation of the draft genome assembly of Paracoccus denitrificans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                         US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Paracoccus
denitrificans PD1222.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
-!- SIMILARITY: Belongs to the cytochrome P450 family.
                                       Parametrical Communications (PD1222).
Bartecia; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Paracoccus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00086; CYTOCHROME P450; UNIXNOWN 1.
Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
SEQUENCE 449 AA; 50659 MW; SF3EEC9E12AA3B35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AAIT01000001; EAN68115.1; -; Genomic_DNA.GO; GO:0020037; F:heme binding; IEA.GO; GO:0005506; F:iron ion binding; IEA.GO; GO:0046872; F:metal ion binding; IEA.GO; GO:0004497; F:monooxygenase activity; IEA.GO; GO:006118; F:lectron transport; IEA.InterPro; IER001128; Cytochrome_P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003, integrated into UniProtKB/TrEMBL 01-JUN-2003, sequence version 1. Fib-2006, entry version 21. Ent-kaurenoic acid oxidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=PD1222;
US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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nes 9; Conservative
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PRINTS; PR00385; P450.
Cytochrome P450.
ORFNames=PdenDRAFT_4722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 ROGRGSVWRFIRDF
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Pfam; PF00067; p450; 1
                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                          NCBI_TaxID=318586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3888;
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                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
MEDLINE=22417727; PubMed=12529541; DOI=10.1104/pp.012963; Davidaon S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.; Davidaon S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.; Plant Physiol. 131:335-344(2003).
-: SUBCELLUGLAR LOCATION: Membrane-bound. Endoplasmic reticulum (By similarity).
-: SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                EMBL, AF537321, AA023063.1; -; MRNA.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:00016020; F:heme binding; IEA.

GO; GO:000497; F:heme binding; IEA.

GO; GO:0004497; F:mencal ion binding; IEA.

GO; GO:0004497; F:monooxygenase activity; IEA.

R GO; GO:000418; P:electron transport; IEA.

R GO; GO:000418; P:electron transport; IEA.

R InterPro; IPR001128; Cytochrome_P450.

R InterPro; IPR00140; EP4501.

R PANTHER; PTHR19383; Cytochrome_P450; 1.

R PANTHER; PR00463; EP450.

R PRINTS; RR00463; EP450.

R PRINTS; PR00464; EP450.

R PROSTIE; PS00066; CYTOCHROME P450; UNKNOWN 1.

R Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding; Monooxygenase; Oxidoceductase.

C SEQUENCE 488 AA; 56478 MW; 503453CB6E43CB30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%; Score 49; DB 2; Length 488; 58.3%; Pred. No. 50; tive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 50.0
Best Local Similarity 58.3
Matches 7; Conservative
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Search completed: May 19, 2006, 14:38:15 Job time : 116.429 secs

S FLGSIWRFIRAF 16 |:|::| |:||| 54 FIGNMWSFLRAF 65

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Sequence 27, Appl Sequence 29, Appl Sequence 15932, A Sequence 2262, Ap

Sequence Sequence Sequence

Sequence

2262, Ap 643, App 3, Appli 3, Appli 3, Appli 3, Appli 2, Appli

Sequence Sequence Sequence Sequence

ALIGNMENTS

Sequence Sequence Sequence Sequence Sequence

```
GENERAL INFORMATION:
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Setul:
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION A-I AGONISTS
TITLE OF INVENTION A-I AGONISTS
TITLE OF INVENTION A-I AGONISTS
TITLE AGONISTS
US-08-132-767-50
US-08-132-767-50
US-09-134-000C-6620
US-10-360-101-83
US-09-609-146-27
US-09-609-146-27
US-09-609-146-27
US-09-609-146-27
US-09-146-27
US-09-146-27
US-08-1480-190-3
US-08-480-190-3
US-08-480-190-2
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US-08-480-190-2
US-08-480-190-2
US-08-480-190-2
US-08-480-190-2
US-08-480-190-2
US-08-480-399A-2
US-08-480-399A-2
US-08-480-399A-2
US-08-480-399A-2
US-08-077-255A-2
US-08-077-255A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTY: USA
ZIP:: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: TESTER: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 30,742
REGISTRENEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRENEY/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX: 660-493-4935
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
SEQUENCE AMINO acids
TURESTER AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: No. 6004925e
US-08-940-095-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
     22
10589
10589
233
441
8122
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144
115
115
115
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                 May 19, 2006, 14:38:42; Search time 24.8571 Seconds (without alignments) 63.384 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 242,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued Patents AA:*
: / FWG Celerra SIDS3/ptodata/2/iaa/5 COMB.pep;*
: / EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep;*
: / EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep;*
: / EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep;*
: / EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep;*
: / EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep;*
: / FMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep;*
: / FMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep;*
: / EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep;*
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                        GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-08-940-093-242
US-08-940-096-242
US-09-465-719-242
US-09-465-719-242
US-09-453-818-242
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US-09-453-818-242
US-09-453-818-242
US-09-453-818-242
US-09-453-814-242
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US-09-453-814-242
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US-09-65-99-242
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US-09-86-980-49
US-09-86-980-49
US-09-880-49
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US-08-318-882-41
US-08-318-882-41
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US-08-318-882-41
US-08-318-882-41
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                                                                                                                                                                                                                                                                                                                                   650591 seqs, 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                - protein search, using sw model
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Maximum DB seq length: 2000000000
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98
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Match Length
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45.5
45.5
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                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                        Searched:
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RESULT 4
US-09-465-719-242
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                                                                                                                      Sequence 242, Application US/08940093
; Sequence 242, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
APPLICANT: Baseux, Jean-Louis
APPLICANT: Bettiner, Klaus
APPLICANT: Babelle
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
TITLE OF INVENTION: ADD THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
Score 78; DB 2; Length 18;
Pred. No. 1.1e-05;
4; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTEX: USA
ZIP: 101046-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIABLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,093
FILING DATE: 29-SEP-1997
CLASSIFICATION ATA:
APPLICATION NUMBER: US/08/10093
FILING DATE: 39-SEP-1997
APPLICATION NUMBER: OPERATION:
NAME: COLUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKT NUMBER: 30,742
REFERENCE/DOCKT NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEX: 66141 PERNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.6%; Score 78; DB 2; I
72.2%; Pred. No. 1.1e-05;
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                                                                            1 GIRRFLGSIWRFIRAFYG 18
 79.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: No. 6037323e
Query Match
Best Local Similarity 72.2'
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 18 amino acids
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Matches 13; Conservative
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-940-093-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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US-08-940-096-242
; Sequence 242, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:

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Sequence 242, Application US/09465719
Sequence 242, Application US/09465719
Patent No. 625377
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Gornit, Isabelle
APPLICANT: Gornit, Isabelle
APPLICANT: Gornit, Gunther
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
APPLICANT: Sekil, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Metz, Cornut, Isabelle
APPLICANT: Metz, Guncher
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
OWNERS OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.6%; Score 78; DB 2; Length 18; 72.2%; Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATIOS SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 39-SEP-1997
CLASSIFICATION NUMBER:
FILING DATE: 30-074:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0005-999
TELECOMMUNICATION INFORMATION:
TELEFAX: 66141 PENNIE
TELEFAX: 66141 PENNIE
TELEFAX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
TURDEMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
TURDEMATION FOR SEQ ID NO: 242:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                         STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6046166e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Conservative
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STATE: NY
COUNTRY: USA
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
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REGISTRATION NUMBER: 30,742
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                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              650-493-5556
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
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STATE:
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Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 78; DB 2; Length 18;
Pred. No. 1.1e-05;
            COMPUTER: EACH COMPUTER:
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
FILING DATE: CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/940,093
APPLICATION NUMBER: 08/940,093
FILING DATE: 29-SER-1997
ATTORNEY AGENT INFORMATION:
NAME: COTLAST, LAURA ATTORNEY COMMUNICATION NUMBER: 009196-0006-999
TELEPHANE: GS0-493-4935
TELEPHANE: 650-493-4935
TELEPHANE: 650-493-556
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASLSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,605
FILING DATE: 26-NO. 632341-1999
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonde LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-423-605-242
US-09-423-605-242
; Sequence 242, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: No. 6265377e
US-09-465-719-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Suture, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Dufourcq, Jean
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APD THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                          Score 78; DB 2; Length 18;
Pred. No. 1.1e-05;
4; Mismatches 1; Indels
009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/ABENT INFORMATION:
NAME: COTUZZI, LAULE A
REGISTRATION NUMBER: 30,742
REEFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: NO. 6329341e; SEQUENCE DESCRIPTION: SEQ ID NO: 242: US-09-453-605-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,838
FILING DATE:
CLASSIPICATION:
PRICR APPLICATION
APPLICATION DATA:
APPLICATION
APPLICATION
APPLICATION
APPLICATION
APPLICATION
APPLICATION
APPLICATION
APPLICATION
APPLICATION NUMBER: 08/940,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEE: Pennie & Edmonds LLP
: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-453-838-242
; Sequence 242, Application US/09453838
: Patent No. 6376464
; GENERAL INFORMATION:
                                          TELEPRONE: 650-493-4935
TELEPRONE: 650-493-5556
TELERA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
     REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GIKKFLGSIWKFIKAFVG 18
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Sequence 242, Application US/09453841
Patent No. 6573239
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650-493-5556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-453-841-242
                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: N
COUNTRY:
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sexul, Renate
APPLICANT: Sexul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Guncher
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: GENE THERAPY APPROACHES TO
TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STRRET: 1155 Avenue of the Americas
                                                                                                                 Gaps
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                                                     Query Match 79.6%; Score 78; DB 2; Length 18; Best Local Similarity 72.2%; Pred. No. 1.1e-05; Matches 13; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: DISACLE
COMPUTER: DISACLE
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: ERESEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,136
FILING DATE: 29-SEP-1997
CLASSIFFCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZI, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0007-999
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-556
TELEPHONE: 650-493-556
TELEPHONE: 650-493-556
TELEPHONE: 650-493-6935
                                                                                                                                                                                                                                                                                                                                US-08-940-136-242
; Sequence 242, Application US/08940136
; Patent No. 6518412
                                                                                                                                                                                                   1 GIKKFLGSIWKFIKAFVG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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US-09-453-841-242
     US-09-453-838-242
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Sequence 242. Application US/09453833
Fatent No. 6602854
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Gentul, Isabelle
APPLICANT: Outure, Klaus
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
PATENT NO. 6573239
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTE: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: DESKETCH
NAME: COMPUTER: DESKETCH
NAME: COMPUTER: DESKETCH
NAME: COMPUTER: DESKETCH
COMPUTER: DESKETCH
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Baseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: APOLIPORED
STREET: 1155 AVENUE & Edmonds LLP
STREET: 1155 AVENUE & Edmonds LLP
STREET: New York
STATE: NY
COUNTEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.6%; Score 78; DB 2; Length 18; 72.2%; Pred. No. 1.1e-05;
                                                                                                                                              ATIONALIA ANGULA ANGULA ANGUELIA ANGUEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY CASHI INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSCQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,840
FILING DATE:
                           APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-453-840-242
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APPLICANT: Beaseux, Jean-Louis
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Gornut, Isabelle
APPLICANT: Gornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCES: 258
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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                                                                                                                                     COUNTRY: USA
ZIP: 10036-281
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATION SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,833
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
TATORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA A
REGISTRATION NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
NAME: COLUZZI, LAURA A
REGISTRATION NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELERHONE: 650-493-4935
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
COMPANION ACIDS
SEQUENCE CHARACTERISTICS:

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COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: SASTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,826
': 1155 Avenue of the Americas
New York
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Patent No. 6630450
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6602854e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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MOLECULE TYPE: No. 6753313e
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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US-10-283-599-242
                                      US-09-453-834-242
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Sekul, Renate
Butther, Klaus
Cornut, Isabelle
Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                         Length 18;
                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTY: VIA

COUNTY: VIA

ZIP: 10036-2811

COMPUTER READABLE FORM:

WEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

COMPUTER: TEM Compatible

COMPUTER: TEM Compatible

OPFRATING SYSTEM: DOS

SOFTWARE: FASKSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/865,989

FILING DATE: 25-May-2001

CLASSIFTCATION: cUnknown>

PRIOR APPLICATION NUMBER: 09/465,719

FILING DATE: 17-DEC-1999

ATTORNEY/AGENT INFORMATION:

NAME: COTUAZI, Laura A

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0006-999

TELLCOMMUNICATION INFORMATION:
                                                                                                                   Query Match 79.6%; Score 78; DB 2; Lei
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
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MOLECULE TYPE: NO. 6734169e

SEQUENCE DESCRIPTION: SEQ ID NO: 242:

US-05-865-989-242
                                                                                                                                                                                                                                                                                                    RESULT 12
US-09-865-989-242
i Sequence 242, Application US/09865989
j Patent No. 6734169
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 650-493-4935
TELEFAX: 650-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                               1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GIRRFLGSIWRFIRAFYG 18
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6716816e
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Best Local Similarity 72.2
Matches 13; Conservative
                                                                              US-09-453-840-242
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Securation 242, Application US/0945334

PREENTAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Beschi, Renal-Louis
APPLICANT: Beschi, Renal-Louis
APPLICANT: Beschi, Renal-Louis
APPLICANT: Beschi, Renal-Louis
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Man History Buttner, Buttn
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Search completed: May 19, 2006, 14:42:56 Job time: 25.8571 secs
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APPLICANT: Sekul, Renate
APPLICANT: Suther, Klaus
APPLICANT: Cornut, Isaballe
APPLICANT: Cornut, Isaballe
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
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     USE TO TREAT DYSLIPIDEMIC DISORDERS. 274
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Pred. No. 1.1e-05;
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TITLE OF INVENTION: USE TO TREAT DYSLIP.
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
STREET: 1155 Avenue of the Americas CITY: New York
STATE: NY
COUNTRY: USA
                                                                                                                                                                                     COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESO VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,599
FILING DATE: 29-CT-2002
CLASSIPICATION THE
APPLICATION NUMBER: 08/940,136
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
TELEPRAY: 650-493-5556
TELEPRAX: 650-493-5556
TELEPRAX: 650-493-5556
TELEPRAX: 650-493-5556
TELEPRAX: 650-493-5556
TELEPRAX: 6141 PENNIE
INFORMATION FOR SED ID NO: 242:
SEGUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TTPE: amino acids
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6844327e
US-10-283-599-242
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Best Local Similarity 72.2%;
Matches 13; Conservative '
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Gaps
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79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels
                      FILING DATE: 17-Dec-1999
CLASSIPECATION:
PRIOR APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
APPLICATION NUMBER: US/08/940,096
FILING DATE: ATORNATION:
NAME: Coruzzi, Laura A
RECISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
RELEPHONE: 650-493-4935
TELLEPAX: 650-493-556
TELLEFAX: 650-493-556
APPLICATION NUMBER: US/09/465,718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GIRRFLGSIWRFIRAFYG 18
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US-09-465-718-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: Bingle
TOPOLOGY: linear
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36, Appl 77, Appl 79, Appl 80, Appl 94, Appl 1100, Appl 97, Appl 242, Appl

OM protein

Run on:

Sequence:

Searched:

Database

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APPLICANT: ANANTHERAMIAH, GATTADAHALLI M.
APPLICANT: GARBER, DAVID W.
APPLICANT: GARBER, DAVID W.
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/10/712,447

PRIOR APPLICATION NUMBER: 00/425,821
PRIOR PELICHING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 2
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: ARABER, DAVID W.
APPLICANT: GARBER, DAVID W.
APPLICANT: DATTA, GETA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILE REFERENCE: 112739-12303
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT APPLICATION NUMBER: US/10/112,447
                                                                                                                                                                                         Sequence Seq
                                                                                                          Sequence
Sequence
Sequence
                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 98; DB 4; Length 18; larity 100.0%; Pred. No. 9.8e-08; Conservative 0; Mismatches n. Talala
US-10-712-447-22

US-10-712-447-78

US-10-712-447-195

US-10-712-447-19

US-10-712-447-58

US-10-712-447-77

US-10-712-447-77

US-10-712-447-79

US-10-712-447-94

US-10-712-447-94

US-10-712-447-97

US-10-712-447-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: c-term amidated US-10-712-447-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 2, Application US/10712447; Publication No. US20040186057A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-712-447-5; Application US/10712447; Sequence 5; Application US/10712447; Publication No. US20040186057A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIRRFLGSIWRFIRAFYG 18
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 18; Conserv
        US-10-712-447-2
              44442222211007777
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102.575 Million cell updates/sec
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                                    GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-712-447-5
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US-10-712-447-121
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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US-10-712-447-10

is Sequence 10, Application US/10712447

publication No. US20040186057A1

general INFORMATION:

APPLICANT: ANATHERAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: WIMBER: US/10/712,447

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

PRIOR PILING DATE: 2002-11-13

**NUMBER OF SEQ ID NOS: 210
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Sequence 8, Application US/10712447

Sequence 8, Application US/10712447

Publication Vo. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: AARBER, DAVID W.

TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES

TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES

TITLE OF INVENTION: 2003-11-13

CURRENT FILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PALENTIN VOY: 3.2

SEQ ID NO 8

LENGTH: 18
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100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels
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100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 60/425,821
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 5
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: ARABER, DAVID W.
APPLICANT: GARBER, DAVID W.
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILE REFERENCE: 112739123US
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT APPLICATION NUMBER: 06/425,821
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE PATENTIN VET: 3.2
SEQ ID NO 13
LENGTH: 18
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US-10-712-47-91
IS SQUENCE 91, Application US/10712447
Publication No. US20040186057A1
GENERAL INFORMATION:
APPLICANT: ANANTHARMIAH, GATTADAHALLI M.
APPLICANT: GARBER, DAVID W.
APPLICANT: DATTA, GERTA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIDOPROTEIN E AND METHODS OF USE
FILE REFERENCE: 11273-123US
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT FILING DATE: 2003-11-13
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100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels
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PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO ED IN SECTION OF THE SECTION OF T
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US-10-712-447-13
Sequence 13, Application US/10712447
Publication No. US20040186057A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 10
LENGTH: 18
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Matches 18, Conservative
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US-10-712-447-129
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US-10-712-447-117
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Sequence 116, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATHARAMIAH, GATTADAHALLI M.

APPLICANT: ANNTHARAMIAH, GATTADAHALLI M.

APPLICANT: ARREER, DAVID W.

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

FILE REFERENCE: 12739-1233

CURRENT FILING DATE: 2003-11-13

RRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PatentIN Ver. 3.2

LENGTH: 18
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US-10-712-447-115

Sequence 115, Application US/10712447

FUBLICARTION OF US20040186057A1

GENERAL INFORMATION

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: ADATBA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APPLICANTION SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

PRIOR PILING DATE: 2003-11-13

PRIOR PILING DATE: 2002-11-13

NUMBER: OF SEQ ID NOS: 210

SOFTWARE: PatentIN Ver. 3.2

SEQ ID NO 115

LENGTH: 18
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                                            ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: peptide
US-10-712-447-91
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORWATION: peptide
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                                                                                                                                              Query Match 96.9%; Score 95; DB 4; Length 18; Best Local Similarity 94.4%; Pred. No. 2.8e-07; Matches 17; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity 88.9
Matches 16; Conservative
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Sequence 117, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANAWTHARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

FILE REFERENCE: 112739-123US

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: Patentin Ver. 3.2

LENGTH. 18
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Fublication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANATHERAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GETA

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

FILE REPERENCE: 112.739-12.30

CURRENT APPLICATION NUMBER: 60/425,821

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: Patentin Ver. 3.2

SEQ ID NO 129

LENGTH: 18
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide US-10-712-447-116
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Pred. No. 3.9e-07;
2; Mismatches 0; Indels
                                                                                                          Length 18
                                                                                                     Query Match 95.9%; Score 94; DB 4; I Best Local Similarity 88.9%; Pred. No. 3.9e-07; Matches 16; Conservative 2; Mismatches 0.
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                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Gaps

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US-10-712-447-53

Sequence 53, Application US/10712447

Publication No. US20040186057A1

Publication No. US20040186057A1

Publication No. US20040186057A1

Publication No. US20040186057A1

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

FILE REFERENCE: 112.73-9-12.34

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT PILING DATE: 2003-11-13

FRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE PATENTIN Ver. 3.2

LENGTH: 18
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US-10-712-447-74

Sequence 74, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:
APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: ARRER, DAVID W.
APPLICANT: BATTA, GETA

TILLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES
CURRENT APPLICATION NUMBER: US/10/712,447

PRIOR FILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENTIN UN VEY: 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 93.9%; Score 92; DB 4; Length 18; Best Local Similarity 88.9%; Pred. No. 7.9e-07; Matches 16; Conservative 2; Mismatches 0; Indels
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  Mismatches
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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16; Conservative
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LOCATION: (3)
OTHER INFORMATION:
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LENGTH: 18
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Sequence 131, Application US/10712447
Sequence 131, Application US/10712447
Publication No. US200401860S7A1
GENERAL INFORMATION:
APPLICANT: APPLICANT: DAVID W.
APPLICANT: DAVID W.
TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILE REPRENCE: 112739-1123US
CURRENT APPLICATION NUMBER: US/10/712,447
PRIOR APPLICATION NUMBER: 00/425,821
PRIOR APPLICATION NUMBER: 60/425,821
PRIOR PILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 131
LENGTH: 18
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Sequence 21, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: BANTHARAMIAH, GATTADAHALLI M.

APPLICANT: BATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

FILE REFERENCE: 12739-1230S

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER: OF SEQ ID NOS: 210

SOFTWARE: Patentin Ver. 3.2

LENGTH: 18
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US-10-712-447-131
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                          Length 18;
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Pred. No. 7.9e-07;
                       Score 94; DB 4; 1 Pred. No. 3.9e-07;
                                                                          2; Mismatches
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ORGANISM: Artificial Sequence
                     Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
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ORGANISM: Artificial Sequence
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Search completed: May 19, 2006, 15:27:57 Job time : 81.2857 secs

1 GIRRFLGSIWRFIRAFYG 18

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RESULT 2
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109, App
70, Appli
48, Appl
48, Appl
545, App
803, App
803, Appl
12, Appl
12, Appl
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Sequence 18, Appl
Sequence 2, Appli
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| EMC Celerra SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
| FEMC_Celerra SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| FEMC_Celerra SIDS3/ptodata/2/pubpaa/US07 NEW_PUB.pep:*
| FEMC_Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| FEMC_Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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17,943 Million cell updates/sec
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                                                                                                                    May 19, 2006, 15:18:37 ; Search time 2.14286 Seconds
                GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-949-925-112

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US-01-302-678-5

US-11-242-505A-48

US-11-242-505A-48

US-11-26-505-948

US-11-169-140-109

US-11-169-140-109

US-11-169-140-109

US-11-204-427-7

US-11-304-129-48

US-11-304-129-40

US-11-304-129-40

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US-11-304-139-40

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US-11-304-149-336

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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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26, Appl
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APPLICANT: Wohlgemuch, Jay
APPLICANT: Wohlgemuch, Jay
APPLICANT: Wooldward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Perentice, James
APPLICANT: MacDonald
APPLICANT: MacDonald
APPLICANT: MacDonald
APPLICANT: MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2003-04-24
PRIOR PILING DATE: 2002-04-24
PRIOR PILING DATE: 2002-04-24
PRIOR PILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: Patentin version 3.2
: SEQ ID NO 2947
LENGTH: 441
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US-11-223-738-6
US-11-324-548-81
US-11-024-548-21
US-11-190-750-135
US-11-264-784-87
US-11-264-784-87
US-10-501-993-26
US-10-501-993-26
US-10-501-993-26
US-10-501-130
US-10-501-120-19
US-10-501-120-19
US-10-501-993-24
US-11-311-55-16
US-11-311-55-16
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US-11-311-55-16
US-11-351-66-44
US-11-251-66-44
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38.3%; Score 37.5; I
Best Local Similarity 33.3%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches
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Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 GLSKFLGTHWLMGNILRLLFG 126
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CORGANISM: Homo sapiens
US-10-511-937-2947
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Sequence 5, Application US/11302678
Publication No. US20060088881A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Siloe-Santiago, Inmaculada
APPLICANT: Soloe-Santiago, Inmaculada
TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: WETHOD BOOK SILOE DISORDERS USING 1435, 559, 34021, 44099, 25278,
TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
FILE REFERENCE: MPI02-012PIRNM_OMNI
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          DB 1; Length 60;
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                                                                       3; Indels
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TITLE OF INVENTION: 67 Human secreted proteins
TITLE OF INVENTION: 67 Human secreted proteins
TITLE REPERENCE: PSO23P2
CURRENT APPLICATION NUMBER: US/09/949,925
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 60/232,150
PRIOR FILING DATE: 1999-01-20
PRIOR FILING DATE: 1999-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PAPLICATION NUMBER: US 60/073,165
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PLING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
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OTHER INFORMATION: Xaa equals stop translation
      Score 36.5; DE Pred. No. 2.2; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 111, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
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          37.2%;
57.1%;
                                                                                                                                           5 FLGSIWRFIRAFYG 18
                                                                                                                                                                                    1| :| |: ||||
31 FLILVWIFV-AFYG 43
      Query Match
Best Local Similarity 57.1:
Matches 8; Conservative
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                           US-09-949-925-111
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US-11-302-678-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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## TITLE OF INVENTION: Methods and Compositions for Treating
### TITLE OF INVENTION: Hematological Disorders Using 212, 2059, 10630, 12848, 13875,
### TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
### TITLE OF INVENTION: 014395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
### CURRENT APPLICATION NUMBER: US, 10/242,505A
### CURRENT FILING DATE: 2005-10-03
### PRIOR FILING DATE: 2002-11-07
### PRIOR FILING DATE: 2001-11-07
### PRIOR PRIOR APPLICATION NUMBER: US 10/320,351
### PRIOR FILING DATE: 2001-12-16
### PRIOR FILING DATE: 2001-12-16
### PRIOR FILING DATE: 2001-12-17
### NUMBER: FastSEQ for Windows Version 4.0
### SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 142, Application US/09949925

Publication No. US20060099575A9

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENITON: 67 Human secreted proteins
FILE REFERENCE: PZ02182

CURRENT APPLICATION NUMBER: US/09/949,925

CURRENT FILING DATE: 2001-09-12

PRIOR APPLICATION NUMBER: US 60/232,150

PRIOR APPLICATION NUMBER: US 60/073,160

PRIOR PELING DATE: 1999-01-27

PRIOR FILING DATE: 1999-01-37

PRIOR FILING DATE: 1998-01-30

NUMBER OF SEQ ID NOS: 298

SEQ ID NO 142

LENGTH: 60
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; OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 37.8
Best Local Similarity 55.6
Matches 5; Conservative
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155 VRRVLGAVW 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo Sapiens
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ORGANISM: Homo sapiens
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GREEAL INCOMPATION:

APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION

APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION

APPLICANT: Browse, John A

APPLICANT: Watts, Jennifer L.

APPLICANT: Watts, Jennifer L.

TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF

TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF

TITLE OF INVENTION: DESATURASES AND METHOD STATY ACIDS

FILE REFERENCE: 4630-58963-02

CURRENT APPLICATION NUMBER: US/10/975,692

CURRENT APPLICATION NUMBER: US/09/9855

PRIOR FILING DATE: 2001-08-17

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1998-12-07

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PARCHIN VERSION 3.3

SECTION OF SEQ ID NOS: 17
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APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prenties, James
APPLICANT: Prenties, James
APPLICANT: Prenties, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REPRENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-12-20
PRIOR FILING DATE: 2002-12-20
PRIOR FILING DATE: 2002-12-20
SOFTWARE: Patentin version 3.2
SEQ ID NO 2540
LENGTH: 351
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46.2%; Pred. No. 44;
tive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                 APPLICANT: EXPRESSION DIAGNOSTICS, INC.
                                                                                                                                                    US-10-511-937-2540
; Sequence 2540, Application US/10511937
; Sublication No. US20060088836A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10975692
Publication No. US20060090221A1
GENERAL INFORMATION:
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      | | | : |||
195 LEEAWSFLDAFY 206
                                                                                                                                                                                                                                                                                                      Wohlgemuth, Jay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 46.2
Matches 6; Conservative
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US-10-511-937-2540
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34.7%; Score 34; DB 7; Length 313;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 36.7%; Score 36; DB 7; Length 599; Best Local Similarity 71.4%; Pred. No. 38; Matches 5; Conservative 2; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/11/302,678
CURRENT FILING DATE: 2005-12-14
PRIOR PILING DATE: 2005-12-14
PRIOR PILING DATE: 2005-01-16
PRIOR PILING DATE: 2000-01-16
PRIOR PILING DATE: 2000-01-18
PRIOR PILING DATE: 2002-02-28
PRIOR PILING DATE: 2002-02-28
PRIOR PILING DATE: 2002-02-28
PRIOR PILING DATE: 2002-03-15
PRIOR PILING DATE: 2002-03-15
PRIOR PILING DATE: 2002-03-15
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-14
PRIOR PILING DATE: 2002-08-14
PRIOR PILING DATE: 2002-08-14
PRIOR PILING DATE: 2002-09-27
PRIOR PILING DATE: 2002-09-27
PRIOR PILING DATE: 2002-10-21
PRIOR PILING DATE: 2002-10-21
PRIOR PILING DATE: 2002-10-21
PRIOR PILING DATE: 2002-11-05
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US-11-242-505A-48
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sequence 40, Application US/11304129
sequence 40, Application US/11304129
publication No. US20060089915A1
GENERAL INFORMATION:
APPLICANT: OHTAKI, Tetsuya
APPLICANT: TAKATSU, Yoshihiro
APPLICANT: TERAO, Yasushi
APPLICANT: TITANO, Yasushi
APPLICANT: SHINTANI, Yasushi
APPLICANT: UNUMBER: US/11/304,129
CURRENT FILING DATE: 2003-09-29
FRIOR FILING DATE: 2003-09-29
FRIOR FILING DATE: 2001-02-02
FRIOR FILING DATE: 2001-02-02
FRIOR FILING DATE: 2001-02-02
FRIOR FILING DATE: 2001-02-02
FRIOR FILING DATE: 2001-07-17
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                                      DB 7; Length 244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.7%; Score 33; DB 7; Length 342; 50.0%; Pred. No. 63;
                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/11204427

Publication No. US20060100146A1

GENERAL INFORMATION:
APPLICANT: Sturley, Stephen L
APPLICANT: Sturley, Define R
APPLICANT: Billheimer, Jeffrey T
APPLICANT: Cromley, Debra

APPLICANT: Cromley, Debra

FILE REFERENCE: 0575/72796/JPW/AJM/JCS

CURRENT APPLICATION NUMBER: US/11/204,427

CURRENT PILING DATE: 2005-08-15

NUMBER OF SEQ ID NOS: 73

SOFFWARE PATENTIN Version 3.3
                               Query Match 34.2%; Score 33.5; D
Best Local Similarity 42.1%; Pred. No. 35;
Matches 8; Conservative 3; Mismatches
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|158 GLVLALGAVWCVARARFIR 176
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Matches 5; Conservative
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84 AIWRQLRDYY 93
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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; ORGANISM: Rat
US-11-304-129-40
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APPLICANT: ARIZEKE PHARMACEUTICALS, INC.

APPLICANT: HOUGYON, Lou, L.

APPLICANT: SHERIDAN, Philip, J.

APPLICANT: HANLEY, Stephen

APPLICANT: GLYNN, Jacqueline, M.

APPLICANT: CHAPIN, Steven

ITLE OF INVENTION: BARRIERS

FILE REFERENCE: 11474-037-999

CURRENT APPLICATION NUMBER: US/11/169,140

CURRENT APPLICATION NUMBER: US 60/246,611

PRIOR APPLICATION NUMBER: US 60/246,819

PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-11-13

PRIOR FILING DATE: 2000-11-13

PRIOR FILING DATE: 2000-11-13

PRIOR FILING DATE: 2000-11-02

PRIOR FILING DATE: 2000-10-02

PRIOR FILING DATE: 2001-10-02

PRIOR FILING DATE: 2001-10-02
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7
Query Match

34.7%; Score 34; DB 6; Length 447;
Best Local Similarity 43.8%; Pred. No. 59;
Matches 7; Conservative 4; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                       Sequence 543, Application US/10505928

Publication No. US20060088532A1

GENERAL INFORMATION:

APPLICANT: Ludwig Institute for Cancer Research et al.

TILLE OF INVENTION: LYPHATIC ENDOTHELIAL GENES

FILE REFERENCE: 28967/39178

CURRENT APPLICATION NUMBER: US/10/505,928

CURRENT PILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: US 60/363,019

PRIOR PILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 866

SOFTWARE: Patentin 3.2

LENGTH: 522
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                                                                                                                                                                                      130 IRKILETIFTILFAFY 145
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                                                                                                                                        2 IRRFLGSIWRFIRAFY 17
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ORGANISM: Homo sapiens
US-10-505-928-543
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RESULT 15
US-10-565-928-853
US-10-565-928-853

i Sequence 853, Application US/10505928

publication No. US20060088532A1

GENERAL INFORMATION:
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

CURRENT APPLICATION NUMBER: US/10/505,928

CURRENT APPLICATION NUMBER: US 60/363,019

PRIOR FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 866

SOFTWARE: PATENTIN 3.2

LENGTH: 1531

TYPE: PRT

CORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: May 19, 2006, 15:28:18 Job time : 2.14286 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 33.7%;
Best Local Similarity 50.0%;
Matches 6; Conservative
339 RYYSSEYHYVGGFYG 353
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APPLICANT: MASUDA, Yasushi
APPLICANT: TAKATSU, Yoshihiro
APPLICANT: WATANABE, Takuya
APPLICANT: TERAO, Yasuko
APPLICANT: SHINDANI, Yasushi
APPLICANT: SHINDANI, Syuji
TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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33.7%; Score 33; DB 6; Length 463;
Best Local Similarity 33.3%; Pred. No. 90;
Matches 5; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 7; Length 393;
Pred. No. 75;
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/0505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US/0709
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SEQ ID NO 545
LENGTH 463
LENGTH 463
    Indels
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    1; Mismatches
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CURRENT APPLICATION NUMBER: US/11/304,129
CURRENT FILING DATE: 2005-12-15
PRIOR APPLICATION NUMBER: US/10/333,192
PRIOR FILING DATE: 2003-09-29
PRIOR FILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-07-18
PRIOR PILING DATE: 2001-02-02
PRIOR PILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: S8
LENGTH: 393
                                                                                                                                                                                    Sequence 48, Application US/11304129
Publication No. US20060088915A1
GENERAL INFORMATION:
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Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                     216 FCGQIWPVDQQFY 228
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; ORGANISM: Homo sapiens
US-10-505-928-545
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Score 33; DB 6; Length 1531; Pred. No. 3.6e+02; 3; Mismatches 3; Indels

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Lecithin: Lecithin:

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Scoring table:

Searched:

Database

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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymotheotide, a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina: low-density lipoprotein; LDL; very low density lipoprotein; LDL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ADO34231 standard; peptide; 18
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87.287 Million cell updates/sec
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Perfect score:
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mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein: E mimicking polypeptide is unseful for reducing aerum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinlemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein (IDL) or very low density lipoprotein (VLDL) to a cell and channees degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein of LDL or mimicking polypeptide of the invention.
apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
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Gaps
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100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 6.4e-08;
                            0; Indels
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                                                            1 GIRRFLGSIWRFIRAFYG 18
               Best Local Similarity 100.
Matches 18; Conservative
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Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide. ADO34225 standard; peptide; 18 AA (first entry) 12-AUG-2004 ADO34225; 

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant, vasotropic, antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia, atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL; very low density lipoprotein; VLDL.

Synthetic

'note= "N-terminal acetyl" Location/Qualifiers /note= "C-terminal Key Modified-site Modified-site

WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. WPI; 2004-411629/38.

Datta G;

Anantharamiah GM, Garber DW,

Claim 4; SEQ ID NO 2; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject

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c (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E c apolipoprotein-E mimicking polypeptide has the following activities: antilippemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is cusful for reducing serum cholesterol in a subject (including a mammal c such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, composatelipoproteinaemia or atherosclerosis; and for reducing the risk of c wycardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking company and enhances binding of low-density lipoprotein (VLDI) to a cell and enhances degradation of LDI, or very low company activity lipoprotein (VLDI) to a cell and enhances degradation of LDI, or very low mimicking polypeptide of the invention.
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cell, a recombinant cell or a transgenic, non-human subject
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 AA;
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mimicking polypeptide encoding polynucleotide; a composition comprising
the synthetic apolipoprotein-E mimicking polypeptide and a carrier;
the synthetic apolipoprotein-E mimicking polypeptide and a carrier;
the synthetic apolipoprotein-E mimicking polypeptide and a carrier;
an monoclonal antibody that specifically binds to the synthetic
continuous polypeptide has the following activities: antilipaemic,
mimicking polypeptide has the following activities: antilipaemic,
cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
cusful for reducing serum cholesterol in a subject (including a mammal
cusful for reducing serum cholesterol in a subject (including a mammal
cusful for reducing serum cholesterol in a subject (including a mammal
cuch as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
chimpanzee or orangutuan); for treating coronary artery disease,
dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
myccardial infarction or stroke; for breaking an embolus in the subject;
and also for treating angina. The synthetic apolipoprotein (LDL) or very low
control of polypeptide enhances binding of low-density lipoprotein (LDL) or sery low
density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
cyclib by a cell. This sequence represents a synthetic apolipoprotein-E
control of the invention. ö (including animal or plant) comprising the synthetic apolipoprotein-E Gaps apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL. . . Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 13. 100.0%; Score 98; DB 8; Length 18; 0; Indels 6.4e-08; Mismatches Pred. No. Anantharamiah GM, Garber DW, Datta G; ADO34236 standard; peptide; 18 AA. ö 1 GIRRFLGSIWRFIRAFYG 18 GIRRFLGSIWRFIRAFYG 18 Query Match
Best Local Similarity 100.0%;
Matches 18; Conservative 0 13-NOV-2003; 2003WO-US036268. 13-NOV-2002; 2002US-0425821P. 12-AUG-2004 (first entry) (UABR-) UAB RES FOUND WO2004043403-A2. Sequence 18 AA; 27-MAY-2004 Synthetic. ADO34236; ADO34236

IID ADO3

XX AC ADO3

XXX ADD3

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c mimicking polypeptide encoding polymucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and can monocolonal antibody that specifically binds to the synthetic apolipoprotein-E apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide is cardiant, vasotropic, antiarteriosolerotic, cerebroprotective, and cardiant, vasotropic, antiarteriosolerotic, cerebroprotective, and cardiant, reducing serum cholesterol in a subject (including a mammal cuseful for reducing serum cholesterol in a subject (including a mammal confinance or orangutan); for treating coronary artery disease, dysbetalipoproteineemia or atherosclerosis, and for reducing the risk of myocardial infarction or stroke, for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking colypeptide enhances binding of low-density lipoprotein (VLDE) to a cell and enhances degradation of LDE or very low cardial properties of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disdase; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic apolipoprotein-E mimicking paptide, SEQ ID No 10.
                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 6.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADO34233 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 AA;
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ADO34233
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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

WPI; 2004-411629/38.

Claim 4; SEQ ID NO 13; 79pp; English.

the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for breaking and for reducing the risk of myocardial infarction or stroke, for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention. low 8888888888888888888888888

Seguence 18 AA;

Gaps ö Length 18; 0; Indels 100.0%; Score 98; DB 8; L 100.0%; Pred. No. 6.4e-08; 0; Mismatches 18 1 GIRRFLGSIWRFIRAFYG Local Similarity 100. es 18; Conservative Query Match Best Loca Matches ద ઠે

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1 GIRRFLGSIWRFIRAFYG 18

ADO34314 standard; peptide; 18

AD034314;

(first entry)

12-AUG-2004

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Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 91.

apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

Synthetic

WO2004043403-A2.

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

Datta G; Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 91; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and 

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypeptide acomposition comprising the synthetic apolipoprotein-E mimicking polypeptide and a composition comprising an monoclonal antibody that specifically binds to the synthetic and

Claim 4; SEQ ID NO 131; 79pp; English.

apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E cardiant, vasotropid, antiarteriosclarotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for treating coronary artery disease, and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein. E mimicking density lipoprotein (UDD) to a cell and enhances degradation of LDL or VUDL by a cell. This sequence represents a synthetic apolipoprotein-E ö Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebkoprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VDDL. Gaps monoclonal antibody that specifically binds to the synthetic ö Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 131. Length 18; Score 95; DB 8; Length 18; Pred. No. 1.8e-07; 1; Mismatches 0; Indels ö mimicking polypeptide of the invention Datta Ā 1 GIRKFLGSIWRFIRAFYG 18 1 GIRRFLGSIWRFIRAFYG 18 ADO34354 standard; peptide; 18 Garber DW, 96.9%; Local Similarity 94.4%; es 17; Conservative 1 13-NOV-2003; 2003WO-US036268. L3-NOV-2002; 2002US-0425821P (first entry) (UABR-) UAB RES FOUND. VPI; 2004-411629/38. Anantharamiah GM, WO2004043403-A2 Sequence 18 AA; 12-AUG-2004 27-MAY-2004. Synthetic. AD034354; Query Match Best Loca Matches RESULT 7 AD034354 0

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apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesteroi in a subject (including a mammal cuchingmanzee or orangutan); for treating oxonary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or atherosclerosis; and for reducing the risk of and also for treating angina. The synthetic apolipoprotein-E mimicking colypeptide enhances binding of low-density lipoprotein (UDD) to a cell and enhances to biding of low-density lipoprotein (UDD) to a cell and enhances degradation of LDL or very low cuching by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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Gaps
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1 GIRRFLGSIWRFIRAFYG 18
                  Conservative
    Query Match
Best Local Similarity
Matches 16; Conserv
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RESULT 8

ADO34338 standard; peptide; 18 AA ADO34338;

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 115. (first entry) 12-AUG-2004

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDL.

Synthetic.

WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

Datta G; Garber DW, Anantharamiah GM,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E minicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 115; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E apolipoprotein-E 

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide and carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic,

Claim 4; SEQ ID NO 129; 79pp; English.

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mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerdtic, cerebroprotective, and antianginal. The synthetic apolipoprotein: mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein.E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VDD) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein.E mimicking mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL;
                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 129.
                                                                                                                                                                                                                                                                   95.9%; Score 94; DB 8; Length 18; 88.9%; Pred. No. 2.6e-07; ive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADO34352 standard; peptide; 18 AA
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                                                                                                                                                                                                                                                                                                                                       1 GIRRFLGSIWRFIRAFYG
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                                                                                                                                                                                                                                                                                                       16; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NO2004043403-A2.
                                                                                                                                                                                                                                         Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is sueful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalioporteinaemia or atherosclerosis, and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
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Length 18; 0; Indels Score 94; DB 8; 1 Pred. No. 2.6e-07; 2; Mismatches 1 GIRRFLGSIWRFIRAFYG 18 95.9%; Local Similarity 88.5 Query Match Matches ò

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Gaps

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18 

RESULT 10 AD034340

ADO34340 standard; peptide; 18 AA. (first entry) 12-AUG-2004 ADO34340; 

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117.

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease, dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

Synthetic.

WO2004043403-A2.

27-MAY-2004

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P.

(UABR-) UAB RES FOUND

Datta G; Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 117; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymucleotide; a composition comprising an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide and actrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide activities; antilipaemic, and antibotic apolipoprotein-E mimicking polypeptide activities; antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

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antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or rangutan); for treading coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (UDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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nes 16; Conservative
                                                                                                                                                                                                                                                                Sequence 18 AA;
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RESULT 11 AD034339

Ä. ADO34339 standard; peptide; 18

ADO34339;

12-AUG-2004 (first entry)

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116.

vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL. apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant;

Synthetic

WO2004043403-A2

27-MAY-2004.

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P.

(UABR-) UAB RES FOUND.

Datta G; Garber DW, Anantharamiah GM,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 116; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypeptide a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic and antibody that specifically binds to the synthetic and antiboprotein-E mimicking polypeptide. The synthetic antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is 

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10%
                     such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanaze or orangutan); for treating coronary artery disease, right special propredentaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (UDL) or very low density lipoprotein (UDL) to a cell and enhances degradation of LDL or VLDL by a call. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
for reducing serum cholesterol in a subject (including a mammal
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Gaps
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  Length 18
                   0; Indels
  Score 94; DB 8; 1
Pred. No. 2.6e-07;
                     2; Mismatches
                                                   1 GIRRFLGSIWRFIRAFYG 18
  95.9%;
88.9%;
95.9
Best Local Similarity 88.9
Matches 16; Conservative
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Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 74.
     ADO34297 standard; peptide; 18 AA.
                (first entry)
                12-AUG-2004
          AD034297;
RESULT 12
   4D034297
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apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDL).

Synthetic

WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P.

(UABR-) UAB RES FOUND.

Datta Anantharamiah GM, Garber DW,

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WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

claim 4; SEQ ID NO 74; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E apolipoprotein-E and activities antilipaemic, cardiant, vasotropic, antiatreriosclerotic, carebroprotective, and antiandinal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; an encoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiateriosclerotic, cerebroprotective, and useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

Claim 4; SEQ ID NO 21; 79pp; English.

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                                                    and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (LDL) or or very low density lipoprotein (LDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 21.
                                                                                                                                                                             Score 92; DB 8; Length 18;
Pred. No. 5.3e-07;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Datta G;
                                                                                                                                                                                                                                                                                                                                              ADO34244 standard; peptide; 18 AA.
                                                                                                                                                                                                                                         18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-NOV-2003; 2003WO-US036268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-NOV-2002; 2002US-0425821P.
                                                                                                                                                                                93.9%;
                                                                                                                                                                                                                                                         1 GIRKFLGSIWRFIKAFYG
                                                                                                                                                                                                                                         1 GIRRFLGSIWRFIRAFYG
                                                                                                                                                                 Query Match
Query Local Similarity 88.5.,
Best Local Similarity 68.5.,
Gonservative
                                                                                                                                                                                                                                                                                                                                                                                                         12-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UABR-) UAB RES FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004043403-A2.
                                                                                                                                                    Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                             AD034244;
                                                                                                                                                                                                                                                                                                                     RESULT 13
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chimpanzee or orangutan); for treating coronary artery disease, dysbetaliapproteinaemia or acherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking oblypopticide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
                                                                                                                                                                                                            mimicking polypeptide of the invention
888888888888
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Gaps
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     5.3e-07;
5.3e-07;
 Length 18;
Query Match 93.9%; Score 92; DB 8; Best Local Similarity 88.9%; Pred. No. 5.3e-07 Matches 16; Conservative 2; Mismatches
                                                       18
                                                                                 18
                                                       1 GIRRFLGSIWRFIRAFYG
                                                                     1 GIRRFLGAIWRFIRSFYG
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Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 53. Ź ADO34276 standard; peptide; 18 (first entry) 12-AUG-2004 ADO34276; RESULT 14 

apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke, embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

Synthetic

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/note= "All Lys residues are DiMethyl-Lysine"
Location/Qualifiers
                      Modified-site
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WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

Datta G; Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 53; 79pp; English

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic and apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities; antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

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antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or with by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypeptide and a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide and a carrier; and amplicating polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dyabetalipoproteinaemia; atherosclerosis: myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic apolipoprotein-E mimicking related R18L linear peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant;
                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                             Score 92; DB 8; Length 18;
Pred. No. 5.3e-07;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADO34227 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                  1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garber DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-NOV-2003; 2003WO-US036268.
                                                                                                                                                                                                                                                                                                                 93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-NOV-2002; 2002US-0425821P
                                                                                                                                                                                                                                                                                                                                                                                                                         1 GIKRFLGSIWRFIKAFYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                          Query Match 93.9
Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anantharamiah GM,
                                                                                                                                                                                                                                                                       Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004043403-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
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useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinsemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (ULD) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
            88888888888888
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ö 0; Gaps Query Match

91.8%; Score 90; DB 8; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 1; Indels

ሯ a Search completed: May 19, 2006, 14:24:30 Job time: 95.2857 secs

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GenCore version 5.1.8 Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

May 19, 2006, 14:24:57; Search time 14.2857 Seconds (without alignments) 121.233 Million cell updates/sec

US-10-712-447-13 98 1 GIRRFLGSIWRFIRAFYG 18 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

-3 -.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	hypothetical prote	transcription regu	2-oxoglutarate/mal	poly (3-hydroxybuty	leucyl-tRNA synthe	leucine-tRNA ligas	acriflavin resista	hypothetical prote	o	hetical pr	NIP1 protein - yea	TMV resistance pro	reverse transcript		c			hypothetical prote	MHC HLA-A cell sur		ě	н	н	HLA-A-0	class I	class I	class I hi	ILA-A2.4a ch	gene HLA-A-0205 pr
071		\$76462	A75578	G64537	A34341	A84060	H64102	AH3568	T32316	B84733	T33269	A46417	T04583	T12085	E84953	T52113	D72540	T15530	B72692	154412	F71707	D97700	нгни69	HLHUA2	I38443	161902	137542	184448	161857	138442
	DB	7	~	Н	~	~	~	0	0	N	N	~	~	~		••	•	7	•	•	~	•		ч				~		7
	Query Match Length	627	178	461	589	908	861	1025	265	489	516	812	1607	407	760	107	214	228	237	246	258	258	273	365	365	365	365	365	365	365
de	Query Match	49.0	45.9	44.9	4.	44.9	44.9	44.4	43.9	43.9	43.9	43.9	43.9	43.4	43.4	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9
	Score	48	45	44		44	44	43.5	43	43	43	43	43	42.5	42.5	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42
			7	m	4	ß	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	leucyl-tRNA synthe	leucyl-tRNA synthe	leucyl-rRNA synthe	leucine-tRNA ligas	homolog to drosoph	hypothetical prote	rfaP protein - Esc	dimethylsulfoxide	hypothetical prote	hypothetical prote	probable permease	hypothetical prote	hypothetical prote	hypothetical prote	cytochrome P450 DW
T04745	AD1282	AH1653	B89961	D69650	T50337	AG2115	C42595	E64109	T20575	AF2599	G97381	T08940	F96571	D96776	T02263
~	N	~	7	~	N	N	N	~	~	~	~	~	7	7	ч
537	803	803	804	804	790	131	265	279	359	364	364	384	406	503	519
42.9	42.9	42.9	42.9	42.9	42.3	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8
42	42	42	42	42	41.5	41	41	41	41	41	41	41	41	41	41
30	31	32	33	34	35	36	37	38	99	40	41	42	43	44	45

## ALIGNMENTS

 RESULT 1 S76462 . hypothetical protein - Synechocystis sp. (strain PCC 6803) . hypothetical protein - Synechocystis sp. G.Species: Synechocystis sp. A;Variety: PCC 6803 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004 C;Accession: S76462 C
 B. Reference number: S74322; MUID:97061201; PMID:8905231 A.Accession: S76462 A.Accession: S76462 A.Status: preliminary A.Molecule type: DNA A.Residues: 1-627 < KAN> A.Residues: 1-627 < KAN> A.Koss-references: UNIPROT:P74489; UNIPARC:UPI00000C103F; EMBL:D90915; GB:AB001339; NID: A.Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
Query Match 49.0%; Score 48; DB 2; Length 627; Best Local Similarity 38.9%; Pred. No. 8.1; Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 Qy         1 GIRRFLGSIWRFIRAFYG 18            :           : :                 Db         597 GLEQLLGKIWQWLRQKFG 614

## RESULT 2 A75578

bable cytochrom	transcription regulator, Mark family - Deinococcus radiodurans (strain R1)
oothetical prote	C;Species: Deinococcus radiodurans
ol protein - yea	C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Ju1-2004
/ resistance pro	C;Accession: A75578
verse transcript	Riwhite, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, K.J.; P
nicillin-binding	, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma)
obable transcrip	S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
octherical prote	Science 286, 1571-1577, 1999
othetical prote	A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
othetical prote	A; Reference number: A75250; MUID: 20036896; PMID: 10567266
HLA-A cell sur	A;Accession: A75578
antiqen export B	A;Status: preliminary
antigen export s	A; Molecule type: DNA
class I histoc	A; Residues: 1-178 < WHI>
class I histoc	A,Cross-references: UNIPROT:Q9RYRO; UNIPARC:UP100000D3BE4; GB:AE001863; GB:AE001825; NID:
ne HLA-A-0203 pr	A;Experimental source: strain R1
C class I histoc	C;Genetics:
C class I histoc	A;Gene: DRA0248
class I histoc	A;Map position: 2

45.9%; Score 45; DB 2; Length 178;

Query Match

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Page

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C;Accession: AH3568
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, A.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc
                                                                                                                                                                                                                                                                              R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and & A; Reference number: A83650; MUID: 20512582; PMID: 11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-806 <STO>
A;Cross-references: UNIPROT:Q9K7S8; UNIPARC:UPI0000136555; GB:AP001518; GB:BA000004; NID:
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Residues: 1-861 <TIGR>
;Cross-references: UNIFROT:P43827; UNIPARC:UP1000013655F; GB:U32774; GB:L42023; NID:9157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20) N;Alternate names: leucyl-tRNA synthetase C;Species: Haemophilus influenzae C;Species: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
                                                                                                                                                                                       C,Species: Bacillus halodurans
C,Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                      eucyl-tRNA synthetase leuS [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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C;Superfamily: leucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 861,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.9%; Score 44; DB 2; 53.8%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 2;
Pred. No. 48;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
100 RRFAGDAWRTNLPYRFAAAFY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: leuS
C;Superfamily: leucine-tRNA ligase
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GAKRFLGRVWNLV 677
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622 GARRFLDRVWRLL 634
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Best Local Similarity 46.2
Matches 6; Conservative
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R; Fleischmann. R.D.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                poly (3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus C; Species: Alcaligenes eutrophus C; Species: Alcaligenes eutrophus C; Species: 2-Jun-1990 #sequence_revision 22-Jun-1990 #sequence_revision 22-Jun-1990 #sequence_revision 22-Jun-1990 #sequence_revision 22-Jun-1990 #sepples, O.P.; Sinskey, A.J. B; Peoples, O.P.; Sinskey, A.J. Biol. Chem. 264, 152598-15333, 1989 A; Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Iden A; Reference number: A34341; MUID:89359357; PMID:2670936
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R Schubert, P.; Krueger, N.; Steinbuechel, A.
J. Bacteriol. 173, 168-175, 1991
A;Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosync
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A;Residues: 1-589 <PEO>
A;Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:g141958; PIDN:
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A,Note: the authors translated the codon TAC for residue 120 as Thr
C,Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC
C,Keywords: acyltransferase
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                                                                                                                                                                                                                                                                                                                                                          Species: Helicobacter pylori
Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
Accession: G64537
                                 Gaps
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A;Cross-references: UNIPARC:UPI0000174217; GB:AE000511; TIGR:HP0143
C;Superfamily: 2-oxoglutarate/malate translocator
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44.9%; Score 44; DB 2; Length 589;
Best Local Similarity 47.6%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 5; Indels
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Pred. No. 26;
2; Mismatches 4; Indels
                                 Indels
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A;Accession: A39190
                                    4;
Pred. No. 7.2;
0; Mismatches
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Best Local Similarity 53.8%;
Matches 7; Conservative
69.2%;
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297 VRRLLSWFWRFVR 309
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                                                                                                2 IRRFLGSIWRFIR 14
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                                 9; Conservative
   Best Local Similarity
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Residues: 1-219 <SCH>
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                                 Matches
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NIPI protein - yeast (Saccharomyces cerevisiae)

N.Alternate names: nuclear import protein; protein YM9924.01c; protein YM9952.11c; protein C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 21-Sep-1993 #sequence revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A46417; S53979; S539702
R;Gu, Z.; Moerschell, R.P.; Sherman, F.; Goldfarb, D.S.
Proc. Natl. Acad. Sci. U.S.A. 89, 10355-10359, 1992
A;Title: NIPl, a gene required for nuclear transport in yeast.
A;Reference number: A46417; MUID:93066237; PMID:1332047
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A;Cross-references: UNIPARC:UPIO000168ACA; EMBL:Z54141; NID:g1072408; PID:g984682; MIPS:)
A;Experimental source: strain AB972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:076442; UNIPARC:UPI000007D477; EMBL:AF068709; PIDN:AAC19257.3 A;Experimental source: strain Bristol N2; clone C24B9
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A,Residues: 571-582,'O',584-640,'K',642,'K',644-812 <CON>
A,Cross-references: UNIPARC:UP10000168ACD; BMBL:Z49212; NID:g798940; PID:g798951; MIPS:YN
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                        P450 homology
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33269
R;Muraxy, J, ;Wohldmann, P.; Langston, Y.; O'Neal, D.
A;Describtion: The sequence of C. elegans cosmid C24B9.
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A;Note: sequence extracted from NCBI backbone (NCBIN:117849, NCBIP:117850)
A;Connor, R.; Churcher, C.M.
Submitted to the EMBL Data Library, April 1995
A;Reference number: S53969
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A;Map position: 2
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome
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                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C24B9.13 - Caenorhabditis elegans
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                 DB 2;
40;
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submitted to the EMBL Data Library, September 1995
A;Reference number: S59302
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A;Map position: 5
A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2
                                                                                                                                          4; Mismatches
                                                                                 Score 43;
Pred. No.
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                                                                                 43.9%;
54.5%;
                                                         Query Match
Best Local Similarity 54.5
Local 6; Conservative
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54 IGNMWSFLRAF
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A;Residues: 1-812 <GU1>
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A; Molecule type: DNA
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Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
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               A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Recension: A43566
A;Scatus: Preliminary
A;Molecule type: DNA
A;Residues: 1-1025 <KUR>
A;Residues: 1-1025 <KUR>
A;Cross-references: WIPPROT: QBYCOS; UNIPARC: UP100000584C8; GB:AE008918; PIDN:AAL53715.1;
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A;Experimental source: strain Bristol N2; clone F31F4
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F31F4.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
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A;Introns: 13/3; 67/2
C;Superfamily: Caenorhabditis elegans hypothetical protein T09F5.1
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R, Blanchard, M.; Kramer, J.; Elliott, G.; Twyman, B. submitted to the EMBL Data Library, September 1997
A; Description: The sequence of C. elegans cosmid F31F4.
A; Reference number: Z21149
A; Accession: T32316
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A;Molecule type: DNA
A;Residues: 1-265 <BLA>
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Pred. No. 22;
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C; Superfamily: hypothetical protein b2075
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531 FLGSVWSFMTLPRSFF 546
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illarity 53.8%;
Conservative ;
      Natl. Acad. Sci. U.S.A. 99,
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 50.03
Matches 8; Conservative
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Best Local Similarity
7; Conserva
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A, Molecule type: DNA
A, Residues: 1-489 <STO>
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                                                                                                                                                                                                                                                                     C;Genetics:
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2; Length 812; Indels

Score 43; DB Pred. No. 66; 4; Mismatches

Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative

|::| ||||: |: 361 GVKRILGSIFSFV 373 1 GIRRFLGSIWRFI 13

g

SGD:S0004926; MIPS:YMR309c

A; Gene: SGD:NIP1 A; Cross-references: A; Map position: 13R

C; Genetics:

5;

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Ratus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-107 <COR>
A;Cross-references: UNIPROT:065154; UNIPARC:UPI000000C45F; EMBL:AF053302; PIDN:AAC08574.1
A;Experimental source: cultivar Columbia
A;Genetics:
A;Gene: KIWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable transcription co-activator KIWI [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004 (Speciesion: T22113 R;Cormack, R.S.; Hahlbrock, K.; Somssich, I.E. Plant J. 14, 685-92, 1998 A;Attle: Isolation of putative plant transcriptional coactivators using a modified two-hy A;Reference number: Z25848; MUID:98346011; PMID:9681033
                                                                                                                                                                                                                            C;Species: Buchnera sp.
C;Daces:02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Acces:02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A!
A;Reference number: A84930; MUID:20445173; PMID:10993077
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A;Cross-references: UNIPARC:UPI00005E4C8; GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
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                                                                                                                                                                                             penicillin-binding protein 1b [imported] - Buchnera sp. (strain APS)
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Pred. No. 13;
2; Mismatches
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43.4%; Score 42.5; I
Best Local Similarity 44.4%; Pred. No. 74;
Matches 8; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: penicillin-binding protein 1B
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32 INRFINGKVWNFPTSIYG 49
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Best Local Similarity 50.0%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: E84953
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A;Molecule type: DNA
A;Residues: 1-1607 <BEV>
A;Cross-references: UNIPROT:065506; UNIPARC:UPI00000AA45C; EMBL:AL022141
A;Experimental source: cultivar Columbia; BAC clone P23E13
B;Bevan, M.; Wedler, H.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schuelle submitted to the Protein Sequence Database, April 1998
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A;Molecule type: mRNA
A;Residues: 1-407 <KIN>>
A;Residues: 1-407 <KIN>>
A;Residues: 1-607 octives: UNIPROT: 022103; UNIPARC: UPI00000AAD3D; EMBL: AB007466; NID: d1170509; A; Experimental source: guard cell protoplasts
C; Superfamily: pol polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TMV resistance protein N homolog F23E13.30 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C;Accession: T05507, T05507 R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse, submitted to the Protein Sequence Database, March 1998 A;Reference number: 215378
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C;Species: Vicia faba (fava bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12085
R;Kinoshita, T.; Wada, H.; Masaaki, I.; Shimazaki, K.
submitted to the EMBL Data Library, September 1997
A;Description: Retrotransposon-like cDNAs from guard cell protoplasts in Vicia faba.
A;Reference number: Z17406
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A; Molecule type: DNA A; Residues: 1448-1607 < BE2> A; Cross-references: UNIPARC: UPI000016DBFD; EMBL: AL022373 A; Experimental source: cultivar Columbia; BAC clone T19K4 C; Genetics: A; Map position: 4 A; Intrans: 1912; 238/2; 556/2; 930/3; 1029/3; 1287/3 A; Note: F23E13.30; T19K4.270

A;Reference number: Z15418 A;Recession: T05507

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Matches

RESULT 13 T12085

ij

Gaps

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Query Match 43.4%; Score 42.5; DB 2; Length 407; Best Local Similarity 57.9%; Pred. No. 40; Matches 11; Conservative 1; Mismatches 4; Indels

1 GIRRFLGSIW---RFIRAF 16

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Eukaryota; Metazoa; Arthropoda; Nexapoda; Insecta; Foelygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
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rhodopseudo
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                                                                                                                 May 19, 2006, 14:13:32; Search time 115.429 Seconds (without alignments) 144.247 Million cell updates/sec
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Q4BFM2 BURVI
Q3PR79 PARDE
Q4EM1 PEA
Q21LN7 9DELT
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Q9F7V7_RHILV
Q44QD1_CHLLI
Q43K01_9CHLB
Q45F7_BURK3
Q45F4_9BURK
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O2JITO_9CYAN
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
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2: uniprot_trembl:*
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Maximum DB seq length: 2000000000
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Query
Match Length DB
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49.0
48.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                          Run on:
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GO:0005524; F:AFP bluding; IEA.
GO:0005524; F:AFPase activity; IEA.
GO:0014626; F:ATPase activity; coupled to transmembrane m. .; IEA.
GO:000106; F:mucleocide binding; IEA.
GO:000106; F:mucleocide binding; IEA.
GO:0008565; F:protein transporter activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                       de Kort C.A.D., Koopmanschap A.B.; "Nucleotide and deduced amino acid sequence of a cDNA clone encoding diapause protein 1, an amylphorin-type storage hexamer of the Colorado
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter A.P., Twelker S., Oresnik I.J., Hynes M.F.;
"Analysis of the genetic region encoding a novel rhizobiocin from
Rhizobium leguminosarum bv. viciae strain 305.";
Can. J. Microbiol. 47.495-502 (2001).
                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=305;
MEDLINE=21360352; PubMed=11467725; DOI=10.1139/cjm-47-6-495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium leguminosarum bv. viciae.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Rhizobiaceae, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                    Query Match 55.1%; Score 54; DB 2; Length 670; Best Local Similarity 43.8%; Pred. No. 11; Matches 7; Conservative 6; Mismatches 3; Indels
Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;
                                                                                                                                                                                                                                                                                                                               670 AA; 79825 MW; 8A000BA115BEC8A6 CRC64;
                                                                                                                                                                         HSSP; P04253; ILL1.

GO; GO:0005344; F:oxygen transporter activity; IEA.

GO; GO:0006810; P:transport; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro; IPR0008203; Hemocyanin.

InterPro; IPR005204; hemocyanin.

PANTHER; PTHR11511; Hemocyanin, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001, integrated into UniProtKB/TrEMBL 01-MAR-2001, sequence version 1. 07-FBB-2006, entry version 25. ABC transporter R2CB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     735 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF273216; AAG25076.1; -; Genomic_DNA.
HSSP; P08716; 1MT0.
                                                                                                                                                                                                                                                                                         PRINTS; PRO0187; HAEMOCYANIN.
PROSITE; PS00210; HEMOCYANIN.2; UNKNOWN.1.
NON TER
1 1 1
SEQÜENCE 670 AA; 79825 MW; 8A000BA115B
                                                                                                    J. Insect Physiol. 40:527-535(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 RHILV
QGF7V7 RHILV PRELIMINARY; PRT;
Q9F7V7;
                                                                                                                                                               EMBL; X76080; CAA53691.1; -; mRNA.
                                                                                                                                                                                                                                                         Pfam; PF03723; Hemocyanin_C; 1.
Pfam; PF00372; Hemocyanin_M; 1.
Pfam; PF03722; Hemocyanin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   351 RKFYGALWSYLRHFFG 366
                                                                                                                                                                                                                                                                                                                                                                                                     3 RRFLGSIWRFIRAFYG 18
                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                       NCBI_TaxID=7539;
                                                                                             potato beetle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=rzcB
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Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequencing of the draft genome and assembly of Chlorobium limicola DSM 245.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Larimer F., Land M.; "Annotation of the draft genome assembly of Chlorobium limicola DSM
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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0440D1;

13-SEP-2005, integrated into UniProtKB/TrEMBL.

13-SEP-2006, sequence version 1.

14-EB-2006, entry version 1.

16-ucyl-tRNA synthetase bacterial/mitochondrial, class Ia.

ORFNames=ClimDRAFT 1980;

Chlorobium limicola DSM 245.

Bacteria; Chlorobia Chlorobiales; Chlorobiaceae;

Chlorobium/Pelodictyon group; Chlorobium.
R GO; GO:0015031; P:protein transport; IEA.

R GO; GO:0005508; P:proteolysis; IEA.

R InterPro; IPR001527; AAA_Arpase.

InterPro; IPR0011527; ABC_TM.

R InterPro; IPR001140; ABC_TM.

R InterPro; IPR001140; ABC_TM.

R InterPro; IPR001140; ABC_TM.

R InterPro; IPR001140; ABC_TM.

R InterPro; IPR001013; Type_I_sec_HyB.

R PANTHER; PTR19242; SF74; Type_I_sec_HyB.

R Pfam; PF00064; ABC_membrane, I.

R Pfam; PF00065; ABC_tran; I.

R Prodom; P0000066; ABC_transporter; I.

R Prodom; P0000066; ABC_transporter; I.

R PROSITE; PS00221; ABC_TMNEPORTER_I; I.

R PROSITE; PS00221; ABC_TRANSPORTER_I; I.

R PROSITE; PS0093; BEC_TRANSPORTER_I; I.

R PROSITE; PS0093; PERTIDASE C39; I.

R PROSITE; PS0093; PERTIDASE C39; I.

R PROSITE; PS0093; PERTIDASE C39; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
InterPro; IPR002302; Leu tRNAsyn_la.
PF00133; tRNA-synt_l; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 53.1%; Score 52; DB 2; Best Local Similarity 62.5%; Pred. No. 26; Matches 10; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 GFRWFLPAIWRYRRAF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GIRRFLGSIWRFIRAF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary data.
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STRAIN=DSM 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
STRAIN=DSM 245;
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                                          22-NOV-2005, integrated into UniProtKB/TrEMBL.
22-NOV-2005, sequence version 1.
21-FBB-21006, entry version 4.
Hypothetical protein.
OrderedLocusNames=Beep18194 A3207;
Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760 / NCIB 9086 / R181941)).
                                                                                                                                                                                                                                                                                                                                US DOE Joint Genome Institute;
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M.,
Vergez L., Schmutz J., Larimer F., Land M., Kyrpides N., Lykidis A.,
Richardson P.;
                                                                                                                                                                                                           Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, Burkholderia, Burkholderia cepacia complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete sequence of chromosome 1 of Burkholderia sp. 383.", submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.0%; Score 51; DB 2; Length 407; 47.1%; Pred. No. 20; 1:ve 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; CP000151; ABB06809.1; -; Genomic_DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;
                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-2005, integrated into UniProtKB/TrEMBL.
13-SEP-2005, sequence version 1.
07-FEB-2006, entry version 2.
407 AA.
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US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q456F4 9BURK PRELIMINARY; PRT; Q456F4;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327 GIRQMLGHVWQWTRSSY 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 47.1%;
les 8; Conservative
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                  NCBI_TaxID=269483;
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  Q39L57_BURS3
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                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US DOE Joint Genome Institute (JGI-PGF);
copbland A., Lucass S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Chlorobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae; Chlorobium/Pelodictyon group; Chlorobium.
                                                                                                               Query Match
Best Local Similarity 61.5%; Pred. No. 29; Length 805;
Matches 8; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-SEP-2005, sequence version 1.
21-FEB-2006, entry version 9.
Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=DSM 266;
US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
Lanctation of the draft genome assembly of Chlorobium phaeobacteroides DSM 266.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phaeobacteroides DSM 266.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AAIB01000002; EAM35935.1; -; Genomic_DNA.
GO; GO:0005224; F:ATP binding; IEA.
GO; GO:0004823; F:Leucine-tRNA ligase activity; IEA.
GO; GO:0006429; F:Leucine-tRNA minoacylation; IEA.
InterPro; IPR002302; Leu tRNASyn_la.
PRUNTS; PR00133; TRNA-synt_l; 1.
PRINTS; PR00985; TRNASYNTHLEU.
TIGRFAMS; TIGR00396; leus_bact; 1.
Aminoacyl-tRNA synthetase.
SEQUENCE 816 AA; 93335 MW; 6770B1DAC50560F1 CRC64;
PRINTS; PR00985; TRNASYNTHLEU.
TIGREPAG; TIGR00396; leus bact; 1.
Aminoacyl-tRNA synthetase.
SEQUENCE 805 AA; 91997 MW; D4F3FE28F9E92DF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.1%; Score 52; DB 2;
61.5%; Pred. No. 29;
ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   13-SEP-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                    816 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORFNames=Cpha266DRAFT_2546;
Chlorobium phaeobacteroides DSM 266.
                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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GISRFLGKVWRLV 634
                                                                                                                                                                                                                                                               622 GISRFLGKVWRLV 634
                                                                                                                                                                                                                     1 GIRRFLGSIWRFI 13
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=290317;
                                                                                                                                                                                                                                                                                                                                                                                 Q43K01 9CHLB
Q43K01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=DSM 266
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Gaps

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                                                                                                                                                                                               STRAIN=AU 1054;
US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                                   Larimer F., Land M.; "Annotation of the draft genome assembly of Burkholderia cenocepacia
                                       07-FEB-2006, entry version 2.

Hypothetical protein.
ORFNames=BcenDRAFT 3751;
Burkholderia cenocepacia, Betaproteobacteria, Broteobacteria, Broteobacteria, Betaproteobacteria, Burkholderiaceae; Burkholderia cepacia complex.
                                                                                                                                                                                                                                                                                                                                                                                                                  AU 1054.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBDJ whole genome shotgun (WGS) entry which
preliminary data.
                                                                                                                                                                                                                                                                                              Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
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RESULT 6 Q39L57\_BURS3

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Name=XKR7; Synonyms=C20orf159, XRG7;
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                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                     'Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                          STRAIN=H12424;
US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
 Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                 02-AUG-2005, sequence version 1.
07-FBB-2006, entry version 2.
Hypothetical protein.
0RFNames=Bcen2424DRAFT 1071;
Burkholderia cenocepacia H12424.
Bacteria; Proteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                             Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.0%; Score 51; DB 2; Length 408; 47.1%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                EMBL; AAH101000010; EAM12352.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 408 AA; 45545 MW; 3C2BCA9471BAAE93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 408 AA; 45603 MW; 7F393888305911D2 CRC64;
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11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
01-MAR-2005, sequence version 1.
07-FEB-2006, entry version 8.
XK-related protein 7.
                                                             Score 51; DB 2;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AAHL01000063; EAM16412.1; -; Genomic_DNA.
                                                                                                                                                                                                        02-AUG-2005, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                   408 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                   5; Mismatches
                                                                                                                                                                                   PRELIMINARY; PRT;
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                                                                                                                      328 GIRQMLGHVWQWTRSSY 344
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328 GIRQMLGHVWQWTRSSY 344
                                                                                                         1 GIRRFLGSIWRFIRAFY 17
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                                                               Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                             NCBI_TaxID=331272;
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=HI2424;
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Q4LK44;
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XKR7_HUMAN
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REDINE_21638749; PubMed=1178052; DOI=10.1038/4148653; RA MEDLINE=21638749; PubMed=1178052; DOI=10.1038/4148653; RA MEDLINE=21638749; PubMed=1178052; DOI=10.1038/4148653; RA Beloukas P., Matthews L.H., Abulust J.L., Burton J., Gilbert J.G.R., Boloukas P., Matthews L.H., Abulust J.L., Burton J., Gilbert J.G.R., Balley J., Bardes R.N., Baddel D.M., Brown A.J., Railey J., Bardes R.N., Barder D.M., Brown A.J., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M., RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Alington A., Coville G.J., Deadman R., Dhami P.D., Dunn M., Railington A.G., Frankland J.A., Fraser A., French L., Garner P., RA Elington A.G., Frankland J.A., Fraser A., Honden P.J., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Johnson D., RA Kay M.P., Kimberley A.M., King A., Knighte A., Laird G.K., Lawlor S., Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McJay R.A., Minstry D., Moore M.J.F., Mullikin J.C., Nickerson T., Rankland E.J., Martin S.L., Patel R., Shownkeen R., Sims S., Swuce C.D., Smith M.L., Scott C.E., Sehra H.K., Shownkeen R., Sins S., Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A., Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A., Mitchead S.L., Whittekeer P., Willey D.L., Walliams L., Williams L., Willing D.K., Willing D.K., Williams L., Wil
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Distributed under the Creative Commons Attribution-NoDerivs License
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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--- SMILARITY: Belongs to the XK family.
--- CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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D8D0FF64B9EDD53D CRC64;
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EMBL; AL031658; CAB88102.1; ALT SEQ; Genomic_DNA.
Ensembl; BNSG000101321; Homo sapiens.
HGNC; HGNC:23062; XKR7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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280 PO
334 PO
404 PO
435 PO
63826 MW; 1
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Nature 414:865-871(2001)
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579 AA;
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-!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
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190 LGQVWRYLRALY 201
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Best Local Similarity
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ID XKR7_RAT
AC Q5GH56;
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                                                                                                                             13-SEP-2005, sequence version 1.
07-FBB-2006, entry version 6.
XK-related protein 7.
Name=XKR7; Synonyms=XRG7;
Pan troglodyres (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euxchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2005, sequence version 1.
07-PEB-2006, entry version 10.
Name=Xkr7; Synonyms=Xkrg7;
Mus musculus (Nouse)
Eukaryota; Merazoa; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Butheria; Burchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                        Huang C.-H., Chen Y.;
"A superfamily of XK-related genes (XRG) widely expressed in vertebrates and invertebrates.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-:- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
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STRAIN=C57BL/6J;
Huang C.-H., Chen Y.;
"A superfamily of XK-related genes (XRG) widely expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50; DB 1; Length 579;
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                11-OCT-2005, integrated into UniProtKB/Swiss-Prot
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                                                                                  579 AA.
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                                                                                                                                                                                                                                                                                                                                                                                         (Potential).
-!- SIMILARITY: Belongs to the XK family.
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NUCLEOTIDE SEQUENCE [MRNA].
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Matches 7; Conservative
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579 AA;
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                                                                                                 Q49LS1;
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DD XKR7 MOUSE
DD XKR7 MOUSE
DT 01-MAR.
DT 01-MAR.
DT 07-PAR.
DT 07-PAR.
DT 07-MAR.
DT 07
                                                    RESULT 10
XKR7_PANTR
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Burchontoglires; dlires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLECTIDE SEQUENCE [MRNA].
STRAIN=Sprague-Dawley;
Huang C.-H., Chen Y.;
"A superfamily of XK-related genes (XRG) widely expressed in vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50; DB 1; Length 580;
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potential.
Potential.
8F4907F391B4F5BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
F3291FABF4C5A826 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2005, integrated into UniProtKB/Swiss-Prot. 01-MAR-2005, sequence version 1. 07-FEB-2006, entry version 8. 07-FEB-2006, entry version 8. Nare-acted protein 7. Name-xKr7; Synonyms-Xrg7; Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XK-related protein 7. /FIId=PRO_0000190791. Potential.
                                                                                                                                                                                                                                           XK-related protein 7./FIId=PRO_0000190789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       580 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 42;
3; Mismatches
                                                                                                                                   EMBL, AYE34253; AATO7102.1; -; mRNA.
Ensembl; ENSMUSG0000042631; Mus musculus.
MGI; MGI:3526711; Xkr7.
Membrane; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Potential).
-!- SIMILARITY: Belongs to the XK family.
(Potential).
-!- SIMILARITY: Belongs to the XK family.
                                                                                                                                                                                                                                                                                                                                           Potential.
Potential.
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Potential.
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07-FEB-2006, entry version 4.
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Q84ZW1_PEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Larimer F., Land M., "Annotation of the draft genome assembly of Burkholderia vietnamiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
Submitted (JUN-2005) to the BMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                Burkholderia vietnamiensis G4.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                      DB 1; Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%; Score 49; DB 2; Length 409; 41.2%; Pred. No. 42; ive 5; Mismatches 5; Indels
                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 409 AA; 45629 MW; CCD3FA52A9F014E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AAEH02000029; EAM28562.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                 13-SEP-2005, integrated into UniProtKB/TrEMBL. 13-SEP-2005, sequence version 1. 07-FEB-2006, entry version 2. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-2005, integrated into UniProtXB/TrEMBL 25-OCT-2005, sequence version 1.
                      Score 50; DB 1
Pred. No. 42;
3; Mismatches
                                                                                                                                                                                                                                                                 409 AA.
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US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                    Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            ORFNames=Bcep1808DRAFT_3388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                   190 LGQVWRYLRALY 201
                                                                                                            6 LGSIWRFIRAFY 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=269482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vietnamiensis G4.
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ID Q3PK79 PARDE
AC Q3PK79,
DT 25-OCT-2005, in
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Vicieae, Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=PD1222;
US DOD Joint Genome Institute (JGI-ORNL);
Latimer F., Land M.;
"Annotation of the draft genome assembly of Paracoccus denitrificans
                                                                                                                                                                                                                                                                    US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Paracoccus denitrificans PD1222.";
Cytochrome P450.

ORFNames=PdenDRAFT 4722;
Paracoccus denltrificans PD1222.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Paracoccus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
Heme; Iron; Metal-binding; Monooxygenase; Öxidoreductase.
SEQUENCE 449 AA; 50659 WW; SF3EEC9E12AA3B35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD1222.";
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AAITO1000001, EAN68115.1; -; Genomic_DNA. GO; GO:0020037; F:heme binding; IEA. GO; GO:0005506; F:iron ion binding; IEA. GO; GO:0046872; F:incn ion binding; IEA. GO; GO:0004197; F:monoxygenase activity; IEA. GO; GO:006118; F:electron transport; IEA. InterPro; IPR001128; Cytochrome_P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0842W17
01-UNY-2003, integrated into UniProtKB/TrEMBL.
01-UNY-2003, sequence version 1.
07-FBB-2006, entry version 21.
Ent-kaurenoic acid oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%; Scor.
64.3%; Pred. No. 40,
... 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    488 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00067; p450; 1.
PRINTS; PR00463; EP4501.
PRINTS; PR00385; P450.
                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE,
STRAIN=PD1222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
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RX MEDLINE=22417727; PubMed=12529541; DOI=10.1104/pp.012963;
RA Davidaon S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.;
RI The pea gene NA encodes ent.kaurenoic acid oxidase.";
RI The pea gene NA encodes ent.kaurenoic acid oxidase.";
Plant Ephysiol. 131:335-344(2003).
C: SUBCELDULAR LOCATION: Wembrane-bound. Endoplasmic reticulum (By similarity).
C: SIMILARITY: Belongs to the cytochrome P450 family.
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Search completed: May 19, 2006, 14:38:12 Job time : 124.429 secs

5.FLGSIWRFIRAF 16 |:|::| |:||| 54 FIGNMWSFLRAF 65

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Patent No. 6004925

GENERAL INFORMATION:

APPLICANT: Deaseux, Jean-Louis

APPLICANT: Buttner, Klaus

APPLICANT: Buttner, Klaus

APPLICANT: Gornut, Isabelle

APPLICANT: Gornut, Isabelle

APPLICANT: Metz, Gunther

APPLICANT: Metz, Gunther

APPLICANT: Metz, Gunther

TITLE OF INVENTION: APDLIPOPROTEIN A-I AGONISTS

TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York
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US-08-132-767-50
US-09-134-000C-6620
US-09-134-000C-6620
US-10-360-101-83
US-09-609-146-27
US-09-609-146-29
US-09-902-540-15932
US-09-902-540-15932
US-09-902-540-15932
US-08-480-190-3
US-08-480-190-3
US-08-480-190-2
US-08-488-379-2
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTWARE: FASISEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-5EP-1997
CLASSIPICATION NUMBER: 30-5EP-1997
FILING DATE: 39-5EP-1997
APPLICATION NUMBER: 09-196-0004-999
RECISTRATION NUMBER: 009196-0004-999
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-556
TELEPAX: 660-493-556
TELEPAX: 6614 PENNIE
INFORMATION FOR SED ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6004925e
US-08-940-095-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
          RESULT 1
US-08-940-095-242
            242, App
892, App
893, App
893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                          May 19, 2006, 14:38:42; Search time 24.8571 Seconds (without alignments) 63.384 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 242,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: /EWG_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PGTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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Sequence
Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                   GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                               650591 segs, 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                               - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                         1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                         US-10-712-447-13
98
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47.5
45.5
45.5
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                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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No.
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APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Gornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: EME COMPATION:
COMPUTER: SHE COMPATION:
COMPUTER: SHE COMPATION:
COMPUTER: SHE COMPATION:
SOFTWARE: FRESEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: COTTAZI, LAUYA A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
RELEPONE: 650-493-4935
TELENDAMINICATION NUMBER: COTTATION NUMBER: CO
Dasseux, Jean-Louis
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-940-096-242
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US-09-465-719-242
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                                                                                                                                                                                                                                                     Sequence 242, Application US/08940093
; Sequence 242, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Battner, Klaus
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                   Score 78; DB 2; Length 18;
Pred. No. 1.1e-05;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.6%; Score 78; DB 2; Length 18; 72.2%; Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: BOS
SOFTWARE: FastSEQ Version 2.0
SOFTWARE: 29-SEP-1997
FILING DATE: 29-SEP-1997
APPLICATION UMBER: ATONER'S ATONER'S ATONER'A COURT INFORMATION:
NAME: COLUZZI, LAUKE A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
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TELERAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                 1 GIKKFLGSIWKFIKAFVG 18
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                                       Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                              1 GIRRFLGSIWRFIRAFYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 72.29
Matches 13, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-940-093-242
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Sequence 242, Application US/09465719
Patent No. 6265377
GENERAL INFORMATION:
APPLICANT: Basseux, Jean-Louis
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                           Length 18;
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1 Similarity 72.2%; Pred. No. 1.1e-05;
13; Conservative 4; Mismatches 1;
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                             1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                     1 GIKKFLGSIWKFIKAFVG 18
                                                                                                     STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6046166e
                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036-2811
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RESULT 3
US-08-940-096-242
US-08-940-096-242
; Sequence 242, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:

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APPLICANT: Dasgeux, Jean-Louis
APPLICANT: Betul, Renate
APPLICANT: Betul Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Octure, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                Query Match

79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels
                  009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIPFICATION
TARGET APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUKE A
REGISTRATION NUMBER: 30,742
REPERENCE/DOCKET UNMBER: 009196-0004-999
TELECOMMUNICATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: NO. 6329341e; SEQUENCE DESCRIPTION: SEQ ID NO: 242: US-09-453-605-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSGQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,838
             REFERENCE/DOCKET NUMBER: 003
TELECOMMUNICATION INFORMATION:
TELEFAX: 650-493-4935
TELEFAX: 650-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acide
TYPE: amino acid
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-453-838-242;
Sequence 242, Application US/09453838
Patent No. 6376664;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 660-493-5556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
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Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PERESON Version 2.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COTUZEI, Laura A
REGISTRATION NUMBER: 30,742
ATTORNEY/AGENT INFORMATION:
NAME: COTUZEI, Laura A
REGISTRATION NUMBER: 009196-0006-999
TELEPHONE: 650-493-556
TELEPHONE: 650-493-556
TELEFRAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTMARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,605
FILING DATE: 26-NO. 6329341-1999
CLASSIFICATION: AUKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: CURKNOWN>
FILING DATE: CURKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 242, Application US/09453605
Patent No. 6329341
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GIRRFLGSIWRFIRAFYG 18
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US-09-465-719-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 72.21
Matches 13; Conservative
  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-453-605-242
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Sequence 242, Application US/09453841

Patent No. 6573239

GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Buttner, Klaus
APPLICANT: Gexul, Renate
APPLICANT: Metrat, Gunther
APPLICANT: Diffourcd, Jean
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
ITTLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 242, Application US/09453833
Sequence 660284
Septent No. 660284
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Buttner, Klaus
APPLICANT: Gornut, Isabelle
APPLICANT: Merz, Gunther, Isabelle
APPLICANT: Merz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 79.6%; Score 78; DB 2; Length 18; Best Local Similarity 72.2%; Pred. No. 1.1e-05; Matches 13; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPANE: 650-493-4935
TELEFAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FESTENG VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,841
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ||::||||||||:||:|| |
| GIKKFLGSIWKFIKAFVG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: No. 6573239e
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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US-09-453-833-242
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                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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GENERAL INFORMATION:
APPLICANT: Bekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Grant, Isabelle
APPLICANT: Grant, Isabelle
APPLICANT: Grant, Jeanelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: GENE THERAPY APPROACHES TO
TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
CORRESPONDENCES: 274
CORRESPONDENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                            Score 78; DB 2; Length 18;
Pred. No. 1.1e-05;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.6%; Score 78; DB 2; Length 18; Best Local Similarity 72.2%; Pred. No. 1.1e-05; Matches 13; Conservative 4; Mismatches 1; Indels
                                                                                                           1; Indels
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30,742
30,742
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OPERATING SYSTEM: DOS
SOFTWAND SYSTEM: DOS
SOFTWAND STATEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,136
FILING DATE: 29-SEP-1997
CLASSIFFICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                     Sequence 242, Application US/08940136
Patent No. 6518412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Coruzzi, Laura A
REGISTRATION UNDRER: 30,742
REFERENCE/DOCKET NUMBER: 0091:
TELECOMMUNICATION INFORMATION:
TELEPAN: 650-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                      1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GIKKFLGSIWKFIKAFVG 18
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                                                               Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 18 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: TRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6518412e
US-08-940-136-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: NY
COUNTRY: USA
ZIP: 10036-211
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                      JS-08-940-136-242
                     US-09-453-838-242
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.US-09-453-841-242
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Gaps

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Pennie & Edmonds LLP

ADDRESSEE:

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Sequence 242, Application US/09453840
; Sequence 242, Application US/09453840
; Patent No. 6716816
; Patent No. 6716816
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Merz, Gunther
; APPLICANT: Merz, Gunther
; APPLICANT: Merz, Gunther
; APPLICANT: Merz, Gunther
; APPLICANT: Diffourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.6%; Score 78; DB 2; Length 18; 72.2%; Pred. No. 1.1e-05;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, LAUYA A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 009196-0004-999
TELECOMMUNICATION INPORMATION:
TELEPHONE: 650-493-556
TELEFAX: 660-493-556
TELEFAX: 660-493-556
TELEFAX: 66141 PENNIE
TELECOMMUNICATION TOR SEQ ID NO: 242:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
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1: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskerte
COMPUTER: IBM Compatible
OFERATING SYSTEM: DOS
SOFTWARE: FASTEMS OF CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,840
FILING DATE:
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-556
TELEPHONE: 650-493-556
TELERAK: 66141 PENNIE
TELERAK: 66141 PENNIE
TELEC CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GIKKFLGSIWKFIKAFVG 18
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                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 18 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: No. 6630450e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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| Sequence 242, Application US/09453826
| Patent No. 6630450
| Patent No. 6630450
| GENERAL INFORMATION:
| APPLICANT: Buttner, Klaus
| APPLICANT: Corntt, Isabelle
| APPLICANT: Dufourcq, Jean
| TILLE OF INVENTION: APPLIPOPROTEIN A-I AGONISTS
| TILLE OF INVENTION: APPLIPOPROTEIN A-I AGONISTS
| TILLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
| NUMBER OF SEQUENCES: 258
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Pennie & Edmonds LLP
| STREET: 1155 Avenue of the Americas
| CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                 COUNTRY: USA

ZIP: 10036-2811
COMPUTER READBALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.6%; Score 78; DB 2; I 72.2%; Pred. No. 1.1e-05; tive 4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTENO VERSION 2.0
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIPICATION:
                : 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GIRRFLGSIWRFIRAFYG 18
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US-09-453-833-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                          USA
                                                                                                             COUNTRY:
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Gaps

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RESULT 14
US-10-283-599-242
US-10-283-599-242
US-10-283-599-242
Sequence 242, Application US/10283599
Patent No. 6844327
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Bettner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Ornut, Isabelle
APPLICANT: Datourcq, Jean
APPLICANT: Datourcq, Jean
APPLICANT: Datourcq, Jean
TITLE OF INVENTION: SUPPLY APPLICANT
TITLE OF INVENTION: SUPPLY APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GIKKFLGSIWKFIKAFVG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                         US-09-453-834-242
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Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                               Query Match 79.6%; Score 78; DB 2; Length 18; Best Local Similarity 72.2%; Pred. No. 1.1e-05; Matches 13; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
(COMPUTER: IBM Compatible
(OPERATING SYSTEM: DOS
SOFTWARE: FESTESQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-M9-2001
CLASSIFICATION CURROWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
NAME: COTUZST, Laura A
REGISTATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION:
TELECOMMUTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6734169e
SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-865-989-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                %30-865-989-242

; Sequence 242, Application US/09865989

; Patent No. 6734169

; GENERAL INFORMATION:

; APPLICANT: Dasseux_ Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAN: 650-493-4935
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GIRRFLGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                        1 GIKKFLGSIWKFIKAFVG 18
                     STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6716816e
US-09-453-840-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
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Sequence 242, Application US/09453834
Sequence 242, Application US/09453834
Sequence 242, Application US/09453834
Septemt No. 675333
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sexul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
THERAPY APPROACHES TO
FENE THERAPY APPROACHES TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         009196-0004-999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036-2811
COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: EN Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESQ Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/45,834
FILING DATE:
PRIOR APPLICATION NUMBER: 08/940,095
FILING DATE:
APPLICATION NUMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAUKA A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 009196-0004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
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Search completed: May 19, 2006, 14:42:54
Job time : 25.8571 secs
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; MOLECULE TYPE: No. 6900177e
US-09-465-718-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Suttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I ACONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
TOWNERS POWDENCES: 228
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
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FITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
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Pred. No. 1.1e-05;
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                                                                                                                                                                              COUNTRY: USAN
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,599
FILING DATE: 29-0CT-2002
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/940,136
FILING DATE: 29-5EP-1997
ATTORNEY/AGENT INFORMATION:
FILING DATE: 30,742
REFERENCE/COCKET NUMBER: 009196-000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 660-493-5556
TELEFAX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
                                                             ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-465-718-242; Sequence 242, Application US/09465718; Sequence 242, Application US/09465718; Patent No. 6900177; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GIKKFLGSIWKFIKAFVG 18
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; MOLECULE TYPE: No. 6844327e
US-10-283-599-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 79.6%;
Best Local Similarity 72.2%;
Matches 13; Conservative
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COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
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Gaps
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79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels
        FILING DATE: 17-Dec-1999
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
APPLICATION NUMBER: 09196-0005-999
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0005-999
TELECOMUNICATION INFORMATION: TELECOMUNICATION INFORMATION: TELEPHONE: 650-493-4935
TELEPHONE: 650-493-5556
TELEPHONE: 650-493-5556
TELEPHONE: 650-493-6556
TELEPHONE: G50-493-6556
TELERY: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242: SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids

LENGTH: 18 amino acids
APPLICATION NUMBER: US/09/465,718
FILING DATE: 17-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GIKKFLGSIWKFIKAFVG 18
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9, Appl 6, Appl 77, Appl 79, Appl 84, Appl 84, Appl 100, App 41, Appl 84, Appl

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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Run on:

Sequence:

Searched:

Database

Result Š.

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APPLICANT: ANANTHERAMIAH, GATTADAHALLI M.
APPLICANT: GARBER, DAVID W.
APPLICANT: DATTA, GEETA

TITLE OF INVENTION: APOLIPPROTEIN E AND METHODS OF USE
TITLE OF INVENTION: APOLIPPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPPROTEIN E AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

PRIOR FILING DATE: 2003-11-13

NUMBER-OF SEQ ID NOS: 210

SEQ ID NO 2: SEQ ID NOS: 210

SEQ ID NO 2: SEQ ID NOS: 210

LENGTH: 18
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Publication US/10712447
Publication No. US20040186057A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: DATTA, GEETA
TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYBEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILE REPERENCE: 112739-123105
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT FILING DATE: 2003-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 100.0%; Score 98; DB 4; Length 18; Similarity 100.0%; Pred. No. 9.8e-08; 18; Conservative 0; Mismatches 0; Indels
US-10-712-447-22
US-10-712-447-18
US-10-712-447-120
US-10-712-447-19
US-10-712-447-56
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US-10-712-447-97
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; OTHER INFORMATION: c-term amidated
US-10-712-447-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/10712447; Publication No. US20040186057A1; GENERAL INFORMATION:
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           Query Match
Best Local S:
Matches 18
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10, Appl
11, Appl
115, App
117, Appl
117, Appl
118, Appl
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1114, Appl
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1116, Appl
1117, Appl
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                                                                                                                                                                                               (without alignments)
102.575 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA Main: *

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: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

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: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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Sequence 8, Ap
Sequence 10, A
Sequence 13, A
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Sequence 129,
Sequence 131,
Sequence 21,
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Sequence 115
Sequence 116
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Sequence 3
Sequence 5
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Sequence 3
Sequence 6
                                                                                                                                                                     May 19, 2006, 15:18:19 ; Search time 81.2857 Seconds
                                 GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-712-447-16
US-10-712-447-18
US-10-712-447-13
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US-10-712-447-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                          - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                           1 GIRRFLGSIWRFIRAFYG 18
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Maximum DB seq length: 200000000
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98
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Match Length
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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Gaps

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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 10
LENGTH: 18
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APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: GARBER, DAVID W.
APPLICANT: CARBER, DAVID W.
APPLICANT: DATTA, GEBTA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILE REPRESENCE: 112739-122US
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT PILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: 60/425,821
BRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: GARBER, DAVID W.
APPLICANT: GARBER, DAVID W.
APPLICANT: DATTA, GBETA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
FILE REFERENCE: 112739-123US
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT FILING DATE: 2003-11-13
PRIOR FILING DATE: 2002-11-13
                                                                                                                                                                                                            FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels
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100.0%; Score 98; DB 4; I
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/425,821
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 5
LENGTH: 18
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US-10-712-447-10
Squence 10, Application US/10712447
Publication No. US20040186057A1
GENERAL INFORMATION:
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                                                                                                                                                                                    ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 8
LENGTH: 18
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US-10-712-447-8
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US-10-712-447-13

Sequence 13, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANNUTHARAMIAH, GATTADAHALLI M.

APPLICANT: ANTHRARMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: APPLICANT SINGLE DOWAIN POLYBEPTIDES MIMICKING

TITLE OF INVENTION: APPLICANT SINGLE DOWAIN POLYBEPTIDES

CURRENT APPLICANT SOURCE: 103-11-13

PRIOR FILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENT VET. SEQ ID NOS: 210

LENGTH: 18

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Publication No. US20040186057A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: ANATHRARMAINH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT APPLICATION NUMBER: 06/425,821

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PALENTI VEF. 3.2

SEQ ID NO 91

LENGTH: 18
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-10-712-447-10
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100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0;
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US-10-712-447-129
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US-10-712-447-117
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US-10-712-447-115

Sequence 115, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHARANIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APPLICANTION: APPLICAN
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Sequence 116, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:
APPLICANT: ANATHRARAMIAH, GATTADAHALLI M.
APPLICANT: DATTA, GEETA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES
TITLE OF INVENTION: APPOLIPOPROTEIN E AND METHODS OF USE
FILE REFERENCE: 112739-123US
CURRENT PILING DATE: 2003-11-13
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
NUMBER: OF SEQ ID NOS: 210
SOOFWARE: Patentin Ver. 3.2
SEQ ID NO 116
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TYPE: PRT
GRGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
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Best Local Similarity 88.9%;
Matches 16; Conservative
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ORGANISM: Artificial Sequence
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Sequence 117, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYMTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: SYMTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: SYMTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLLEPPROFICIEN E AND METHODS OF USE

FILE REFERENCE: 112739-123US

CURRENT APPLICATION NUMBER: 2003-11-13

PRIOR APPLICATION NUMBER: 60/425,821

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APPLICANT: GARBER, DAVID W.
APPLICANT: GARBER, DAVID W.
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
TILE REPERRORE: 1127391303
CURRENT APPLICATION NUMBER: 105/112,447
CURRENT APPLICATION NUMBER: 60/425,821
PRIOR FILING DATE: 2003-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PATENTIN VOY: 3.2
SOFTWARE: PATENTIN VOY: 3.2
LENGTH: 18
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: peptide US-10-712-447-116
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Pred. No. 3.9e-07;
2; Mismatches 0; Indele
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Pred. No. 3.9e-07;
2; Mismatches 0;
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Best Local Similarity 88.9%;
Matches 16; Conservative 2
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9%;
Matches 16; Conservative
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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 117
LENGTH: 18
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Mismatches
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: (Dime) Lys
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16; Conservative
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NAME/KEY: MOD_RES
LOCATION: (3)
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LENGTH: 18
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Publication No. US20040186057A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

FILE REFERENCE: 112739-12308

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT APPLICATION NUMBER: 06/425,821

PRIOR RILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: Patentin Ver. 3.2

LENGTH. 18
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Sequence 21, Application NO US20040186057A1

SEDEMAL INFORMATION:
APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: DATTA, GEETA
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
STILE REPERENCE: 112739-123US
CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PARCENTIN VOICE: 3.2

SEQ ID NO 2: LENGTH: 18
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US-10-712-447-131
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US-10-712-447-21
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Pred. No. 7.9e-07;
                   Score 94; DB 4; Length 18;
Pred. No. 3.9e-07;
2; Mismatches 0; Indels
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                                                                                                    1 GLRRFLGSIWRFLRAFYG 18
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                     Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity
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US-10-712-447-131
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APPLICANT: GARBER, DAVID W.
APPLICANT: GARBER, DAVID W.
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
TITLE OF INVENTION: APOLICATION WUMBER: US/10/712,447
CURRENT APPLICATION WUMBER: US/10/712,447
PRIOR APPLICATION WUMBER: 60/425,821
PRIOR APPLICATION WUMBER: 60/425,821
PRIOR APPLICATION WUMBER: 60/425,821
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PATENTIN VEY: 3.2
SEQ ID NO 74
LENGTH: 18
Sequence 53, Application US/1071247
; Sequence 53, Application US/1071247
; Sequence 53, Application US/2040186057A1
; GENERAL INCORNATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; CURRENT FILING DATE: 2003-11-13
; CURRENT FILING DATE: 2003-11-13
; RILOR APPLICATION NUMBER: 60/425,821
; RILOR APPLICATION NUMBER: 60/425,821
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE PARCELIN VEY: 3.2
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US-10-712-447-4

i Sequence 4, Application US/10712447

i Publication No. US20040186057A1

i GENERAL INFORMATION:
    APPLICANT: ANATHARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

ITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES MIMICKING

ITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

PRIOR FILING DATE: 2003-11-13

PRIOR FILING DATE: 2003-11-13

SOFTWARE: PATENTIN NUMBER: 60/425,821

PRIOR FILING DATE: 2003-11-13

SOFTWARE: PATENTIN NUMBER: GAGUENCE

SOFTWARE: PATENTINE:

CHERT INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide

US-10-712-447-4
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Best Local Similarity 94.4%; Pred. No. 1.6e-06;
Matches 17; Conservative 0; Mismatches 1; Indels
                                                                              Query Match 93.9%; Score 92; DB 4; Length 18; Best Local Similarity 88.9%; Pred. No. 7.9e-07; Matches 16; Conservative 2; Mismatches 0; Indels
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1 GIRKFLGSIWRFIKAFYG 18
; OTHER INFORMATION: peptide US-10-712-447-74
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Search completed: May 19, 2006, 15:27:56 Job time : 81.2857 secs

1 GIRRFLGSIWRFIRAFYG 18

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Sequence 2947, Application US/10511937

Publication No. US2006008836A1

GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Woldgemuth, Jay
APPLICANT: Woris, MacDonald
APPLICANT: Ly, Ngoc
APPLICANT: Porentice, James
APPLICANT: Rosenberg, Steven
JITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITION FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFRENCE: 506612000104
CURRENT FILING DATE: 2004-10-19
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: Patentin Version 3.2
SOFTWARE: Patentin Version 3.2
LENGTH: 441
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US-11-223-738-6
US-11-312-958-48
US-11-024-5448-21
US-11-190-750-135
US-11-264-784-87
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US-10-504-193-26
US-10-504-193-26
US-10-504-193-26
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         US-11-242-505A-18
         RESULT 2
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1. /EWC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2. /EWC Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3. /EWC Celerra_SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:*

4. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/FOR_NEW_PUB.pep:*

5. /EWC Celerra_SIDS3/ptodata/2/pubpaa/US08 NEW_PUB.pep:*

6. /EWC_Celerra_SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*

7. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*

8. /EWC_Celerra_SIDS3/ptodata/2/pubpaa/US11 NEW_PUB.pep:*
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                                                                                                                                                                                                                        May 19, 2006, 15:18:37 ; Search time 2.14286 Seconds (without alignments) 17.943 Million cell updates/sec
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                                         GenCore version 5.1.8 Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-342-505A-18

US-11-242-505A-18

US-11-242-505A-18

US-11-242-505A-18

US-11-269-140-109

US-11-169-140-109

US-11-169-140-109

US-11-204-427-7

US-11-304-129-48

US-11-304-129-48

US-11-304-129-48

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US-11-304-129-48

US-11-304-129-48

US-11-304-129-48

US-11-304-129-48

US-11-304-13-48

US-11-104-54A-169

US-11-204-427-1

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US-11-204-65-18
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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RESULT 5
US-11-302-678-5
US-11-302-678-5
Sequence 5, Application US/11302678
; Sequence 5, Application US/11302678
; Sequence 5, Application No. US2006008881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: G41, 260, 55089, 21407, 42032, 46656, 65553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 11237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPIO2-012P1RNM_OWNI
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         Length 60;
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    Score 36.5; DB 1;
Pred. No. 2.2;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: 67 Human secreted proteins TITLE OF INVENTION: 67 Human secreted proteins FILE REFERENCE: P2023P2
CURRENT APPLICATION NUMBER: US/09/949,925
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 60/232,150
PRIOR FILING DATE: 1990-01-20
PRIOR FILING DATE: 1990-01-20
PRIOR FILING DATE: 1990-01-30
PRIOR FILING DATE: 1990-01-30
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PRIOR FILING DATE: 1990-01-30
NUMBER OF SEQ ID NOS: 290
SOFFWARE: PALENTIN VET. 2.0
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; OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-111
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Publication No. US20060099575A9
GENERAL INFORMATION:
         Query Match 37.2%;
Best Local Similarity 57.1%;
Matches 8; Conservative
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-949-925-111
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TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 14717, 9941, 19310,
TITLE OF INVENTION: Hamatological Disorders Using 232, 2059, 10630, 14717, 9941, 19310,
FILE REFERENCE: MIZOOL-288PRRCPLOWING
CURRENT PILING DATE: 2005-10-03
FRIOR PILING DATE: 2005-11-07
FRIOR PILING DATE: 2001-11-07
FRIOR FILING DATE: 2001-11-07
FRIOR PILING DATE: 2001-11-17
FRIOR APPLICATION NUMBER: US 10/320,351
FRIOR FILING DATE: 2001-12-16
FRIOR FILING DATE: 2001-12-16
FRIOR FILING DATE: 2001-12-16
FRIOR FILING DATE: 2001-12-16
FRIOR FILING DATE: 2001-12-17
FRIOR FILING DATE: 2001-12-17
FRIOR FILING DATE: 2001-12-17
FRIOR APPLICATION NUMBER: 06/341,606
FRIOR FILING DATE: 2001-12-17
FRIOR FILING DATE: 2001-13-17
FRIOR FRIOR
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37.8%; Score 37; DB 7; Length 403;
Best Local Similarity 55.6%; Pred. No. 16;
Matches 5; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 142, Application US/09949925

Publication No. US2060099575A9

GENERAL INPORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 67 Human secreted proteins
FILE REFERENCE: PZ021P2

CURRENT APPLICATION NUMBER: US/09/949,925

CURRENT APPLICATION NUMBER: US 60/232,150

PRIOR PRIOR PELICATION NUMBER: US 60/232,150

PRIOR PELING DATE: 1999-01-20

PRIOR FILING DATE: 1999-01-30

PRIOR FILING DATE: 1999-01-30

PRIOR PELING DATE: 1999-01-30

PRIOR FILING DATE: 1999-01-30

PRIOR DATE: 1999-01-30

PRIOR PRI
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NAME/KEY: SITE

LOCATION: (60)

OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-142
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155 VRRVLGAVW 163
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US-11-242-505A-18
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ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/11/302,678 CURRENT FILING DATE: 2005-12-14

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GENERAL INCRMATION:

APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION

APPLICANT: Browse, John A

APPLICANT: Browse, John A

APPLICANT: Watts, John A

APPLICANT: Watts, John Is, James G

APPLICANT: Watts, John Is, James G

APPLICANT: Watts, John Is SATURABES AND METHODS OF USING THEM FOR SYNTHESIS OF

TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS

TILLE OF INVENTION: DESATURABES: US/10/975,692

CURRENT PILNO BATE: 1094-10-26

CURRENT APPLICATION NUMBER: US 09/857,583

PRIOR FILING DATE: 2001-08-17

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1998-12-07

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PATENTIN VERSION 3.3

SOFTWARE: PATENTIN VERSION 3.3
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                                                                                                                                                                                                                                                                    APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Prentice, James
APPLICANT: Prentice, James
APPLICANT: Prentice, James
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-12-20
PRIOR FILING DATE: 2002-12-20
PRIOR FILING DATE: 2002-12-20
PRIOR FILING DATE: 2002-12-20
SOSTWARE: Patentin version 3.2
SEQ ID NO 2540
LENGIH: 351

**LENGIH: 351
**LENGIH: 351
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Pred. No. 44;
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2; Mismatches
                                                                                                                                                                                                              APPLICANT: EXPRESSION DIAGNOSTICS, INC. APPLICANT: Wohlgemuth, Jay
                                                                                                 US-10-511-937-2540
; Sequence 2540, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10975692 Publication No. US20060090221A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Caenorhabditis elegans
US-10-975-692-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.7%;
Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 LGTVWLKEMLFYG 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 447
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APPLICANT: Carroll, Joseph M.
APPLICANT: Healy, Alleen
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
FILE REFERENCE: MPISOR-28BPIRCPIOWNIM
CURRENT APPLICATION NUMBER: US/1/242,505A
CURRENT FILING DATE: 2005-10-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
36.7%; Score 36; DB 7; Length 599;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 0; Indels
PRIOR PAPLICATION NUMBER: 2005-12-14
PRIOR FILING DATE: 2003-01-16
PRIOR FILING DATE: 2003-01-16
PRIOR FILING DATE: 2003-01-16
PRIOR PELING DATE: 2002-01-18
PRIOR PELING DATE: 2002-01-18
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-03-15
PRIOR PELING DATE: 2002-03-15
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-09-17
PRIOR FILING DATE: 2002-09-27
PRIOR FILING DATE: 2002-09-27
PRIOR FILING DATE: 2002-09-27
PRIOR FILING DATE: 2002-09-27
PRIOR FILING DATE: 2002-10-21
PRIOR FILING DATE: 2002-10-21
PRIOR FILING DATE: 2002-10-27
PRIOR FILING DATE: 2002-11-05
PRIOR FILING DATE: 2002-11-05
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FASTEED FOR WINDOWS Version 4.0
SEQ ID NO 5
LENGTH: 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 10/290,078
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2002-12-16
PRIOR FILING DATE: 2002-12-16
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-242-505A-48
; Sequence 48, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
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US-11-242-505A-48
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US-11-302-678-5
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                     Length 244;
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Pred. No. 75;
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                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                Sequence 7, Application US/11204427
; Sequence 7, Application US/11204427
; Publication No. US20060100146A1
; GENERAL INFORMATION:
   APPLICANT: Sturley, Stephen L
; APPLICANT: Billheimer, Jeffrey T
APPLICANT: Cronley, Debra
; TITLE OF INVENTION: AMAT-RELATED METHODS AND ARTICLES
; FILE REFERENCE: 0575/72796/JPW/AJM/JCS
; CURRENT APPLICATION NUMBER: US/11/204,427
; CURRENT FILING DATE: 2005-08-15
; NUMBER OF SEQ ID NOS: 73
; COFTWARE: PatentIn version 3.3
                          DB 7;
                        Score 33.5; DE Fred. No. 35; 3; Mismatches
                                                                                                                                                                                158 GLVLALGAVWCVARARFIR 176
                                                                                                                             1 GIRRFLGSIW----RFIR 14
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                        Query Match
Best Local Similarity 42.1%;
Matches 8; Conservative
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Matches 5; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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ORGANISM: Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-11-304-129-40
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APPLICANT: SHERIDAN, Philip, J.
APPLICANT: SHERIDAN, Philip, J.
APPLICANT: HAUSTON, Lou, L.
APPLICANT: HARLEY, Stephen
APPLICANT: HARLEY, Stephen
APPLICANT: CHAPIN, Jacqueline, M.
APPLICANT: CHAPIN, Steven
TILLE OF INVENTION: METHERS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CF
TILLE OF INVENTION: METHERS: US/11/169,140
CURRENT FILING DATE: 2005-06-27
FRIOR FILING DATE: 2001-02-09
FRIOR FILING DATE: 2000-11-14
FRIOR FILING DATE: 2000-11-14
FRIOR FILING DATE: 2000-11-14
FRIOR FILING DATE: 2000-11-14
FRIOR FILING DATE: 2000-11-02
FRIOR FILING DATE: 2000-10-02
FRIOR FILING DATE: 2000-10-02
FRIOR FILING DATE: 2000-10-02
FRIOR FILING DATE: 2001-0-02
FRIOR FILING DATE: 2001-0-09-06
FRIOR FILING DATE: 2001-10-02
FRIOR APPLICATION NUMBER: 09/969,748
FRIOR FILING DATE: 2001-10-02
FRIOR FILING DATE: 2001-10-02
FRIOR FILING DATE: 2001-10-02
FRIOR PRICERTING DATE: 2001-10-02
FRIOR FILING DATE: 2001-10-02
FRIOR 
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34.7%; Score 34; DB 6; Length 447; 43.8%; Pred. No. 59; Live 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.7%; Score 34; DB 6; Length 522; 47.1%; Pred. No. 70; tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LOUGHING INStitute for Cancer Research et al.
TILE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE PATENTIN 3.2
LENGTH: 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 109, Application US/11169140
Publication No. US20060099150A1
GREERAL INFORMATION:
APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                   Sequence 543, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
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130 IRKILETIFTILFAFY 145
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                                                                                                        2 IRRFLGSIWRFIRAFY 17
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Best Local Similarity 47.11
Matches 8; Conservative
     Query Match
Best Local Similarity 43.8<sup>†</sup>
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: Homo sapiens
US-10-505-928-543
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US-11-169-140-109
                                                                                                                                                                                                                                      RESULT 9
US-10-505-928-543
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US-11-169-140-109
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339 RYYSSEYHYVGGFYG 353

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GENERAL INFOGRATION

GENERAL INFOGRATION

APPLICANT: MASUDA, Yasushi

APPLICANT: MATANDE, Yasushi

APPLICANT: MATANDE, Yasushi

APPLICANT: MATANDE, Yasushi

APPLICANT: TERAO, Yasushi

APPLICANT: TERAO, Yasushi

APPLICANT: TERAO, Yasushi

APPLICANT: TERAO, Yasushi

APPLICANT: HINUMA, Syuji

TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof

FILE REFERENCE: 2762180P

CURRENT APPLICATION NUMBER: US/11/304,129

CURRENT FILING DATE: 2005-12-15

PRIOR APPLICATION NUMBER: US/10/333,192

PRIOR FILING DATE: 2000-07-18

PRIOR FILING DATE: 2000-07-18

PRIOR FILING DATE: 2001-02-02

PRIOR FILING DATE: 2001-02-02

PRIOR FILING DATE: 2001-07-17

NUMBER OF SEQ ID NOS: 58

LENGTH: 393

LENGTH: 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 33.7%; Score 33; DB 7; Length 393; Best Local Similarity 46.2%; Pred. No. 75; Matches 6; Indels Matches 6; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39170 ENDOTHELIAL GENES
FURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR PILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PRECENTIN 3.2
LENGTH: 463
  9
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 545, Application US/10505928; Publication No. US20060088532A1; GENERAL INFORMATION;
                                                                                                                                                                                                           Sequence 48, Application US/11304129
Publication No. US20060088915A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 FCGOIWPVDQQFY 228
                                                                                        216 FCGQIWPVDQQFY 228
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                                             5 FLGSIWRFIRAFY 17
6; Conservative
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US-10-505-928-545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Mouse US-11-304-129-48
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  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 6; Length 1531;
Pred. No. 3.6e+02;
3; Mismatches 3; Indels
RESULT 15
US-10-505-928-853

US-10-505-928-853

Sequence 853, Application US/10505928

Publication No. US20060088532A1

GENERAL INFORMATION:

TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

FILE REFERENCE: 2896/39178

CURRENT APPLICATION NUMBER: US/10/505,928

CURRENT FILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: US 60/363,019

PRIOR FILING DATE: 2002-03-07

NUMBER OF SEG ID NOS: 866

SOFTWARE: PATENTIN 3.2

LENGTH: 1531
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Job time : 3.14286 secs
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Local Similarity 50.0%;
nes 6; Conservative
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1122 LGLIYFFVQRFY 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LGSIWRFIRAFY 17
                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-505-928-853
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Matches
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May 19, 2006, 14:13:22 ; Search time 94.2857 Seconds (without alignments) 87.287 Million cell updates/sec
GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                     2589679 seqs, 457216429 residues
                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                  1 GLRRFIGSIWRFIRAFYG 18
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98
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Perfect score:
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_8:\*
1: geneseqp1980s:\*
2: geneseqp1990s:\*
3: geneseqp2000s:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp2001s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:\*

geneseqp2005s:\*

## SUMMARIES

	uol	Synthetic																						
	Description	Ado34338	Ado34339	Ado34231	Ado34354	Ado34225	Ado34228	Ado34236	Ado34340	Ado34233	Ado34350	Ado34314	Ado34352	Ado34297	Ado34244	Ado34276	Ado34227	Ado34335	Ado34322	Ado34336	Ado34337	Ado34241	Ado34240	Ado34344
		ADO34338	ADO34339	ADO34231	ADO34354	ADO34225	AD034228	ADO34236	ADO34340	ADO34233	ADO34350	ADO34314	ADO34352	ADO34297	ADO34244	AD034276	ADO34227	ADO34335	ADO34322	ADO34336	ADO34337	ADO34241	ADO34240	ADO34344
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	Query Match Length DB	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18
مد (	Match	100.0	100.0	95.9	95.9	95.9	95.9	95.9	95.9	95.9	95.9	92.9	91.8	89.8	89.8	89.8	87.8	87.8	86.7	85.7	85.7	85.7	84.7	84.7
	Score	96	98	94	94	94	94	94	94	94	94	91	90	88	88	88	98	86	85	84	84	84	83	83
	Kesuit No.	-	7	М	4	S	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

Ado34284 Synthetic Ado34305 Synthetic	33			Ado34301 Synthetic	Ado34343 Synthetic	Ado34318 Synthetic		Ado34279 Synthetic	Ado34303 Synthetic	Ado34242 Synthetic	Ado34300 Synthetic	_	Ado34317 Synthetic		Ado34280 Synthetic	4	Ado34342 Synthetic	Ado34320 Synthetic	Aay18917 Lecithin:	Aay19171 Lecithin:
3 ADO34284 3 ADO34305	3 ADO34239	3 ADO34319	3 ADO34245	3 ADO34301	3 ADO34343	3 ADO34318	3 ADO34302	3 ADO34279	3 ADO34303	3 ADO34242	3 ADO34300	3 ADO34281	3 ADO34317	3 ADO34323	3 ADO34280	B ADO34264	B ADO34342	3 ADO34320	2 AAY18917	2 AAY19171
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22.5	5 <u>6</u>	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

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Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 115. Ä ADO34338 standard; peptide; 18 (first entry) 12-AUG-2004 ADO34338; ADO34336 

apolipoprotein-E mimicking polypeptide, antilipaemic, cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina. low-density lipoprotein; LDL; very low density lipoprotein; LDL.

Synthetic.

WO2004043403-A2.

27-MAY-2004.

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P.

(UABR-) UAB RES FOUND.

ö Datta Garber DW, Anantharamiah GM,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 115; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypeptide and comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic

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apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal cuseful for reducing serum cholesterol in a subject (including a mammal chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or atherosclerosis; and for reducing the risk of and also for treating angina. The synthetic apolipoprotein-E mimicking colypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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Gaps
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0
100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 5.2e-08;
                            0; Indels
                              0; Mismatches
                                                                            1 GLRRFIGSIWRFIRAFYG 18
                                                           1 GLRRFIGSIWRFIRAFYG 18
              Best Local Similarity 100.
Matches 18; Conservative
 Query Match
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Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116. ADO34339 standard; peptide; 18 AA. (first entry) 12-AUG-2004 ADO34339; RESULT 2 ADO34339 

apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vaeotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

Synthetic.

WO2004043403-A2 27-MAY-2004 13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P.

(UABR-) UAB RES FOUND

Datta G; Garber DW, Anantharamiah GM,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treatir coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 116; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E apolipoprotein-E

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic,

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             cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E minicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinnemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E minicking polypopride enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VDDL) to a cell and enhances degradation of LDL or very low density lipoprotein (VDDL) to a cell and enhances degradation of LDL or very low density lipoprotein (VDDL) by a cell. This sequence represents a synthetic apolipoprotein-E
                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL; very low density lipoprotein; VLDL.
mimicking polypeptide has the following activities: antilipaemic,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 8.
                                                                                                                                                                                                                                                                                               ch 100.0%; Score 98; DB 8; Length 18; I Similarity 100.0%; Pred. No. 5.2e-08; 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                             mimicking polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; SEQ ID NO 8; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADO34231 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                    1 GLRRFIGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                            1 GLRRFIGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-NOV-2002; 2002US-0425821P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-NOV-2003; 2003WO-US036268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anantharamiah GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004043403-A2.
                                                                                                                                                                                                                                                                  Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AD034231;
                                                                                                                                                                                                                                                                                                                                          Matches
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cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
                    88888888888888888888
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ö 95.9%; Score 94; DB 8; Length 18; 88.9%; Pred. No. 2.1e-07; 0; Indels 2; Mismatches 1 GLRRFIGSIWRFIRAFYG 18 Best Local Similarity 88.9 Matches 16; Conservative Query Match ò

; 0

Gaps

ADO34354 standard; peptide; 18 AA. ADO34354; 

12-AUG-2004 (first entry)

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 131

apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; seroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; ULDL.

Synthetic.

WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P.

(UABR-) UAB RES FOUND

Datta G; Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 131; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising

Claim 4; SEQ ID NO 2; 79pp; English.

ö antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanase or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein (LDL) or very low density lipoprotein (MDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein. E mimicking mimicking polypeptide of the invention. Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide. Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL; Gaps ö Length 18; 0; Indels 95.9%; Score 94; DB 8; I 88.9%; Pred. No. 2.1e-07; iive 2; Mismatches 0; 'note= "N-terminal acetyl" /note= "C-terminal amide" ö Datta Location/Qualifiers ADO34225 standard; peptide; 18 AA 18 1 GLRRFIGSIWRFIRAFYG 18 Garber DW, 13-NOV-2003; 2003WO-US036268. 13-NOV-2002; 2002US-0425821P. 1 GLRRFLGSIWRFLRAFYG (first entry) 16; Conservative (UABR-) UAB RES FOUND WPI; 2004-411629/38. Local Similarity Anantharamiah GM, WO2004043403-A2 Sequence 18 AA; Key Modified-site Modified-site 12-AUG-2004 27-MAY-2004 Synthetic. AD034225; Query Match Matches CCCCCCX8XX1414X8XX8X6X6X6X6X141414X88X8X6X6X6X6X6X6X6X6X6X 8888888888888888 g ð

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the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for breaking and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (LDL) or or orlub by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
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95.9%; Score 94; DB 8; Length 18; 88.9%; Pred. No. 2.1e-07; Ui-marrhes 0; Indels
                                                                                            18
                                                                  1 GLRRFIGSIWRFIRAFYG 18
                                                                              Query Match 95.9
Best Local Similarity 88.9
Matches 16; Conservative
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Gaps

ADO34228 standard; peptide; 18 ADO34228; RESULT 6 ADO34228

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(first entry) 12-AUG-2004 

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 5.

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; servoke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

Synthetic

WO2004043403-A2

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

Datta G; Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 5; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymocleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic

an monoclonal antibody that specifically binds to the synthetic
apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
cc aminicking polypeptide has the following activities: antilippemic,
c cardiant, vasotropic, antiarteriosolarotic, cerebroprotective, and
cc antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
cu seful for reducing serum cholesterol in a subject (including a mammal
c such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
c chimpanzee or orangutan); for treating coronary artery disease,
cc dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
myocardial infarction or stroke; for breaking an embolus in the subject;
and also for treating angina. The synthetic apolipoprotein-E mimicking
cc polypeptide enhances binding of low-density lipoprotein (LDL) or very low
cdensity lipoprotein (VLDL) to a cell and enhances degradation of LDL or
c winicking polypeptide of the invention. ö Gaps apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDL. Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis .. 0 Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 13. 2.1e-07; Length 18; Score 94; DB 8; Pred. No. 2.1e-07 2; Mismatches ö Claim 4; SEQ ID NO 13; 79pp; English. Datta Ź coronary artery disease, dysbetal comprises an amino acid sequence. ADO34236 standard; peptide; 18 18 18 Garber DW, 95.9%; 13-NOV-2002; 2002US-0425821P 13-NOV-2003; 2003WO-US036268 1 GLRRFIGSIWRFIRAFYG (first entry) Local Similarity 88.5 es 16; Conservative (UABR-) UAB RES FOUND WPI; 2004-411629/38. Anantharamiah GM, WO2004043403-A2. Sequence 18 AA; 12-AUG-2004 Synthetic. AD034236; Query Match Matches RESULT 7 ADO34236 \$

mimicking polypeptide has the following activities: antilipaemic,

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apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or atherosclerosis; and for reducing the risk of and also for treating angina. The synthetic apolipoprotein-E mimicking colypeptide enhances binding of low-density lipoprotein (ULDL) to a cell and enhances lost and coll and enhances of LDL or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                         Score 94; DB 8; Length 18;
Pred. No. 2.1e-07;
2; Mismatches 0; Indels
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Best Local Similarity 88.9
Matches 16; Conservative
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      cardiant, vasotropic, antiarterioscierotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is subsetul for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetaliopproteinaemia or atherosclerosais, and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptides activities: antilipaemic,
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Pred. No. 2.1e-07;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                 95.9%;
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                                                                                                                                                                                                                                                                               Sequence 18 AA;
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antianginal. The synthetic apolipoprotein-E minicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinsemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E minicking density lipoprotein (VLDL) to a cell and enhances degradation of LDL or very low VLDL by a cell. This sequence represents a synthetic apolipoprotein-E minicking minicking polypeptide of the invention. vasotropic, antiarteriosclerotic, cerebroprotective, and Sequence 18 AA; 888888888888888888

Gaps ö 95.9%; Score 94; DB 8; Length 18; 88.9%; Pred. No. 2.1e-07; ive 2; Mismatches 0; Indels 18 1 GLRRFIGSIWRFIRAFYG Best Local Similarity 88.5 Matches 16, Conservative Query Match ઠે

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ADO34350 standard; peptide; 18 AA. (first entry) 12-AUG-2004 ADO34350; RESULT 10 ADO34350 

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 127.

apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL;

Synthetic

WO2004043403-A2.

27-MAY-2004

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

Datta G; Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 127; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polygeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymuclectide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

ö antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol ih a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein-E mimicking density lipoprotein (VLDL) to a cell and enhances degradation of LDL or wLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention. apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL. Gaps ö Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 91. Score 94; DB 8; Lengtn 10, Pred. No. 2.1e-07; 2; Mismatches ö Datta ADO34314 standard; peptide; 18 AA. 1 GLRRFIGSIWRFIRAFYG 18 18 Garber DW, 13-NOV-2003; 2003WO-US036268. 95.9%; 13-NOV-2002; 2002US-0425821P 1 GLRRFIGSLWRFLRAFYG (first entry) Best Local Similarity 88.9 Matches 16; Conservative (UABR-) UAB RES FOUND. Anantharamiah GM, WO2004043403-A2 Sequence 18 AA; 12-AUG-2004 27-MAY-2004. Synthetic, AD034314; Query Match RESULT 11 AD034314 g 8888888888888888 ò

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypeptide and a comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and apolipoprotein-E mimicking polypeptide and a carrier; and apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide and the following activities: antilipaemic, cardiant, vasotropic, antiatteriosclerotic, carebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis Claim 4; SEQ ID NO 91; 79pp; English. comprises an amino acid sequence.

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cuch as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinsemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (IDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
useful for reducing serum cholesterol in a subject (including a mammal
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   Score 91; DB 8; Lens-
Pred. No. 6.2e-07;
O: Indels
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                                               1 GLRRFIGSIWRFIRAFYG 18
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Best Local Similarity 83...
Best Local 15; Conservative
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ADO34352 standard; peptide; 18 AA RESULT 12 ADO34352

ADO34352; 

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 129.

12-AUG-2004 (first entry)

väsotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterot; coronary artery disease; dysbetalipoproteinaemia; atherosclerosts; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL. apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant;

Synthetic

WO2004043403-A2.

27-MAY-2004

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND.

Datta G; Garber DW, Anantharamiah GM,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 129; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-buman subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymoleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities antilipeanic, cardiant, vasotropic, antiatteriosclerotic, carebroprotective, and antiandinal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal

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cuch as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosedlerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (UDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
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                                                                                                                                               Sequence 18 AA;
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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein. E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide, a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and custing polypeptide apolipoprotein-E mimicking polypeptide apolipoprotein-E mimicking polypeptide as the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and useful for reducing serum cholesterol in a subject (including a mammal cuch as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, claim 4; SEQ ID NO 74; 79pp; English.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymuclectide, a composition comprising an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiatreriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is cuseful for reducing serum echolesterotic (including animals such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease,
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chimpanzee or orangutan); for treating coronary artery disease, dysbetalioproteinaemia or atherosclerosis, and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking oblypaptide enhances binding of low-density lipoprotein (ULD) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholestrent, coronary artery disease, dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis
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                                                                                                                                                                                                                    Length 18;
                                                                                                                                                                                                   89.8%; Score 88; DB 8; Ler
77.8%; Pred. No. 1.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Datta G;
                                                                                                                                      mimicking polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; SEQ ID NO 21; 79pp; English.
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                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                       ADO34244 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anantharamiah GM, Garber DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-NOV-2003; 2003WO-US036268.
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Best Local Similarity
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                                                                                                                                                                             Sequence 18 AA;
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dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein.E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein.E mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypeptide and a comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and a monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and apolipoprotein-E mimicking polypeptide and the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, carebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
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/note= "All Lys residues are DiMethyl-Lysine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 53.
                                                                                                                                                                                              Score 88; DB 8; Length 18;
Pred. No. 1.8e-06;
4; Mismatches 0; Indels
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Local Similarity 77.8%;
les 14; Conservative '
                                                                                                                                                                                                                                                                          1 GLRRFIGSIWRFIRAFYG
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1 GIRRFLGAIWRFIRSFYG
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                                                                                                                                                            Sequence 18 AA;
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useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein. E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein. E mimicking mimicking polypeptide of the invention.
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Best Local Similarity 77.8%; Pred. No. 1.8e-06;
Matches 14; Conservative 4; Mismatches 0; Indels

1 GLRRFIGSIWRFIRAFYG 18 |::||:||||||||||| 1 GIKRFLGSIWRFIKAFYG 18

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Search completed: May 19, 2006, 14:24:31 Job time : 94.2857 secs

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GenCore version 5.1.8 Copyright (c) 1993 - 2006 Biocceleration Ltd.
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						ALIGNMENTS	
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• •	1 9 9 6 6	: 25-Apr-1997 # :: 25-Apr-1997 # :ssion: 876462 :ko, T.; Sato, S Okumura, S.; S	997 #8 462 to, S.	#sequence_re S.; Kotani, Shimpo, S.;	ii.	revision 25-Apr-1997 #text_cha , H.; Tanaka, A.; Asamizu, E.; ; Takeuchi, C.; Wada, T.; Wata	_change 09-Jul-2004 E.; Nakamura, Y.; Miyajima, N.; Watanabe, A.; Yamada, M.; Yasuda,
* .	A,Title: Se	equenc	e analysis er S74322	/Bis	the	genome of the unicellular 97061201; PMID:8905231	cyanobacterium Synechocystis
	A.Accession: S76462 A.Status: preliminary A.Molecule type: DNA A.Residues: 1-627 KAN>	1: S76 prelim type: 1-62	462 inary DNA 7 < KAN	Cad	744	: INTPARC: UPI 00000C103F:	EMBL: D90915; GB: AB001339; NID:
	A;Note: th	a nucl	eotide	sequen	i g	s submitted to the EMBL C	June 1996
	Query Matc Best Local Matches		Similarity 7; Conser	49.0% larity 38.9% Conservative	56	Score 48; DB 2; Lengun Pred. No. 8.2; 6; Mismatches 5; Inde	v 00
	yo da	1 GL    597 GL	RRFIGS ::  EQLLGK	GLRRFIGSIWRFIRAFYG    : :    ::  GLEQLLGKIWQWLRQKFG	FYG :-	. 18 : 614	
	RESULT 2						
	hypothetical C;Species: C C;Date: 29-0	al pro Caeno -Oct-1	protein C enorhabdi t-1999 #8	C24B9.13 itis ele sequence	gan	bditis elegans 9-Oct-1999 #text_	change 09-Jul-2004
	C;Accession: T33269 R;Murray, J; Wohldmann, P.; Langston, Y R;bmitted to the EMBL Data Library, May A;Description: The sequence of C. elegan	n: T33 J.; Wo to the ion: T	269 hldman EMBL	n, P.; Data Li	Lar Ibra	gston, Y.; O'Neal, D. ry, May 1998 elegans cosmid C24B9.	
	A) RELECTED A) ACCEBBION A) Status: ] A) Molecule	n: T33 prelim type:	269 inary; DNA	trans	late	d from GB/EMBL/DDBJ	
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	A;Generics A;Gene: CE A;Map posi	SP:C24 tion: 13/3;	.B9.13 5 67/2;	116/2;		8/2; 315/2; 364/2	

48.0%; Score 47; DB 2; Length 516; 52.9%; Pred. No. 9.8;

Query Match Best Local Similarity

N

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A; Molecule type: mRNA
A; Residues: 9-120, M'.122-365 <CASI>
A; Cross-references: UNIPARC:UPI00001737ED; EMBL:X57954; NID:g32150
A; Note: this allele is designated A*0204
A; Note: the sequence in GenBank entry HSHLAA020, release 106.0, (PID:g32151) differs becs
R; Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 28-Feb-1980 #sequence_revision 22-Apr-1995 #text_change 08-Dec-2000
C;Accession: I55948; E35997; Ā02191; S19020; S77965; S23593; A93834; A93919; S14802; A021
R;Koller, B.H.; Orr, H.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPARC:UPI0000124E24; GB:M84379; GB:M32322; NID:g403143; PIDN:AAAS96A;Note: this allele is designated A*0201 (previously HLA-A2.1)
R;Krangel, M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Unusual RNA splicing generates a setreted form of HLA-A2 in a mutagenized B lymm
A;Reference number: A02191; MUID:85230571; PMID:3874058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-365 <KOL>
A; Residues: 1-365 <KOL>
A; Cross-references: UNIPARC:UP10000124E24; GB:K02883; NID:g187605; PIDN:AAA98727.1; PID:A; Cross-references: Uymphoblastoid cell line 721
A; Experimental source: 1ymphoblastoid cell line 721
R; Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
R; Ennis, P.D.; Zemmour, J.; A. R. T. 2833-2837, 1990
A; Title: Rapid cloning of HAA-A, B cDNA by using the polymerase chain reaction: frequency A; Reference number: A35997; MUID:90207291; PMID:2320591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Immunol. 134, 2727-2733, 1985
A;Title: Cloning and complete sequence of an HLA-A2 gene: Analysis of two HLA-A alleles
A;Reference number: 155948; MUID:85132727; PMID:2982951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            class I histocompatibility antigen HLA-A2 alpha chain precursor [validated] - human
                                                                                                                                                                                                                                                                                                                          Aintrons: 89/3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen
F;195-260/Domain: immunoglobulin homology <IMM>
F;85/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                              class I molecules
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Pred. No. 16;
                                                                                A,Accession: B24671
A,Molecule type: DNA
A,Residues: 1-273 <HOLD-
A,Cross-references: UNIPROT:P10316; UNIPARC:UPI0000124E4B
C,Genetics: A,Gene: GB:HLA-A
A,Cenes: CFB:HLA-A
A,Cross-references: GDB:119310; OMIM:142800
A,Map position: 6p21.3-6p21.3
EMBO J. 4, 2849-2854, 1985
A;Title: Exon shuffling in vivo can generate novel HLA 6
A;Reference number: A91021; MUID:86055720; PMID:3877632
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A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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Best Local Similarity
Matches 6; Conserv
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A, Molecule type: mRNA
A, Residues: 1-365 < ENN>
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A64420; MUID:20083487; PMID:10617197
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C; Keywords: surface antigen
F;101-166/Domain: immunoglobulin homology < IMM>
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R;Arnot, D.; Lillie, J.W.; Auffray, C.; Kappes, D.; Strominger, J.L.
Immunogenetics 20, 237-252, 1984
A;Title: Inter-locus and intra-allelic polymorphisms of HLA class I antigen gene mRNA. A;Reference number: I54412; MUID:84287690; PMID:6332068
A;Accession: I54412
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-246 ares.
A;Cross-references: UNIPROT:Q29945; UNIPARC:UPI000088A27D; GB:M27537; NID:g187727; PIDN
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A;Status: preliminary
A;Nolecule type: DNA
A;Molecule type: DNA
A;Residues: 1-489 <STO>
A;Cross-references: UNIPROT:Q9ZV72; UNIPARC:UPI00009D8ED; GB:AE002093; NID:g3831452;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
                                                                                                                                                                                                                                                             probable cytochrome P450 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84733
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C;Spacies: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
   Gaps
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      Indels
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MHC HLA-A cell surface antigen - human (fragment)
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Pred. No. 14;
4; Mismatches
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   Mismatches
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                                                                                                                  252 LKFFITSLWMFMHAFDG 268
                                                          2 LRRFIGSIWRFIRAFYG 18
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   Conservative
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|GNMWSFLRAF
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R; Holmes, N.; Parham, P.
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Best Local Similarity
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A;Map position: 2
C;Superfamily: Svn
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PID:

Accession: S23593

A; Accession: A93834

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"HC class I histocompatibility antigen HLA-A2 alpha chain (allele A*0216) precursor - hun Cispecies: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C;Accession: 137542; 84958.
Immunogenetics 41, 388, 1995
A;Ritle: Identification of a novel HLA-A2 subtype, HLA-A*0216.
A;Reference number: 137542; MUID:95278976; PMID:759139
A;Accession: 137542
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Variety: isolate A*012 c;Datety: isolate A*0212 d;Datety: isolate A;Belich, M.P.; Mature 357, 326, 329, 1992 d;Datety: isolatety: isola
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A;Cross-references: UNIPARC:UPI000016AD39; dB:M84378; NID:g187625; PIDN:AAA59604.1; PID:ç
A;Experimental source: cell line KRC 033; 180late A*0212
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F)1-24/Domain: signal sequence #status predicted <SIG>
F)25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predic
F;220-285/Domain: immunoglobulin homology <IMM>
                                                                                                                                                     Fibolmes, N.; Ennis, P.; Wan, A.M.; Denney, D.W.; Parham, P.
J. Immunol. 139, 936-941, 1987
A;Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A28
A;Reference number: 138441; MUID:87252273; PMID:3496393
A;Accession: 138443
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIRARC:UP1000016A06EB; EMBL:U03863; NID:9432438; PIDN:AAA03604.1; PII C;Superfamily: class I histocompatibility antigen; immunoglobulin homology F;220-285/Domain: immunoglobulin homology <IMM>
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                   Č;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: 138443
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A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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Pred. No. 21;
4; Mismatches 2; Indels
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Pred. No. 21;
4; Mismatches
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A;Molecule type: mRNA
A;Residues: 1-365 <RES>
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    gene HLA-A-0203 protein - human
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127 VGSDWRFLRGYH 138
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 25-85, RXXX., 90-94,'AH', 97,'V', 99-112,'Z',114-118,'LZ',121-125,'X',127-131,'
A; Residues: 25-85, RXXX., 90-94,'AH', 97,'V', 99-112,'Z',114-118,'LZ',121-125,'X',127-131,'
A; Residues: 25-85, EX, 267-294 < CLOP>
A; Cross-references: UNIPARC: UPI00001737EF
R; Silver, M.L.; Parker, K.C.; Wiley, D.C.
R; Silver, M.L.; Parker, K.C.; Wiley, D.C.
A; Aille: Reconstitution by MHC-restricted peptides of HLA-A2 heavy chain with beta-2-mic
A; Reference number: S14802; MUID: 91204056; PMID: 2017257
                                                                                                                                                                                                                                                                                                           A; Cross-references: UNIPARC:UP10000124E24; EMBL:M84379; NID:g403143; PIDN:AAA59606.1; PI A; Cross-references: UNIPARC:UP10000124E24; EMBL:M84379; NID:g403143; PIDN:AAA59606.1; PI A; Experimental source: cell line GRC 138; isolate A*0201
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
Immunogenetics 35, 344-346, 1992
A;Title: Structure of the HLA-A *0211 (A2.5) subtype: further evidence for selection-dribA;Reference number: $23593; MUID:92218010; PMID:1559719
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A;Cross-references. GDB:13-6p21.3
A;Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1; 365/1
A;Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1; 365/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Superfamily: class I histocompatibility antigen; transmembrane protein; transplantati
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-165/Product: WHC class I histocompatibility antigen HLA-A2 alpha chain #status expe
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A; Residues: 9-96, ID., 99-365 < CAS2>
A; Residues: 9-96, ID.), 99-365 < CAS2>
A; Cross-references: UNIPARC: UPI000008AF57; EMBL: X60764; NID: 932156; PIDN: CAB56609.1; 1
A; Note: this allele is designated A*0211 (previously HLA-A2.5)
B; Note: his allele is designated A*0211 (previously HLA-A2.5)
B; Note: H.T.; Lopez de Castro, J.A.; Parham, P.; Ploegh, H.L.; Strominger, J.L.
B; Ort., H.T.; Lopez de Castro, J.A.; Parham, P.; Ploegh, H.L.; Strominger, J.L.
A; Note: Natl. Acad. Sci. U.S.A. 76, 4395-4399, 1979
A; Title: Comparison of amino acid sequences of two human histocompatibility antigens, A; Reference number: A93834; MUID: 80056745; PMID: 92029
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F;220-285/Domain: immunoglobulin homology <IPM>
F;220-231/Domain: intransmembrane #status predicted <TPM>
F;32-365/Domain: intracellular #status predicted <IPM>
F;32-365/Domain: intracellular #status predicted <INT>
F;110/Binding site: carbohydrate (Asn) (Covalent) #status experimental F;125-188,227-283/Disulfide bonds: #status predicted
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Nature 357, 326-329, 1992
A;Title: Unusual HiA-B alleles in two tribes of Brazilian Indians.
A;Reference number: 137120; MUID:92269955; PMID:1317015
A;Accession: S77965
                                                                                                                                                                    A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: mRNA A;Residues: 1-365 <BEL>
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Pred. No. 21;
4; Mismatches 2; Indels
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Cross-references: UNIPARC:UPI00001737F0

A, Gene: GDB: HLA-A

Molecule type: protein Residues: 25-36 <SIL>

Accession: S14802

44.9%;

Local Similarity hes 6; Conserv

:|| |||:| VGSDWRFLRGYH 138

127

Gaps

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A.Residues: 1-219 <SCH>
A.Residues: 1-219 <SCH>
A.Cross-references: UMIPARC:UPI000016E162; GB:M64341; NID:g141964; PIDN:AAA21979.1; PID:g
A.Note: the authors translated the codon TAC for residue 120 as Thr
C.Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC
                                                                                                                                                                                                                                                                                                                                                                                                                                R.Holmes, N.; Ennis, P.; Wan, A.M.; Denney, D.W.; Parham, P.
J. Immunol. 139, 936-941, 1987
A;Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A28
A;Reference number: 138441; MUID:87252273; PMID:3496393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Alcaligenes eutrophus
C;Date: 22-Jun-1990 #sequence_revision 22-Juh-1990 #text_change 09-Jul-2004
C;Date: 22-Jun-1990 #sequence_revision 22-Juh-1990 #text_change 09-Jul-2004
C;Accession: A34341, A35190
B;Peoples, O.P.; Sinskey, A.J.
J; Biol. Chem. 264, 15298-15303, 1989
A;File: Poly-beta-hydroxybutyrate (PHB) biobynthesis in Alcaligenes eutrophus H16. Ident
A;Reference number: A34341; MUID:89359357; PMID:2670936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-589 cPEO-
A;Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:g141958; PIDN:
A;Experimental source: strain H16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-365 <RES>
A;Cross-references: UNIPROT:P01892; UNIPARC:UPI000016A06D; EMBL:U03862; NID:g432436; PIDN
A;Cross-references: UNIPROT:P01892; UNIPARC:UPI000016A06D; EMBL:U03862; NID:g432436; PIDN
C;Superfamily: class I histocompatibility ancigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>
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J. Bacteriol. 173, 168-175, 1991
A;Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynth
                                                                                                                                                                                                                                                                                                             gene HLA-A-0205 protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul.1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I38442
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47.6%; Pred. No. 34;
tive 0; Mismatches 5; Indels
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                                5;
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Pred. No. 21;
   Pred. No. 21;
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Best Local Similarity 50.0%;
Matches 6; Conservative
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127 VGSDWRFLRGYH 138
                                                                                                                                                   127 VGSDWRFLRGYH 138
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: 18448
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residuss: 1-365 «RES>
A;Cross-references: UNIPARC:UPI000016AD38; GB:M84377; NID:g187623; PIDN:AAA59603.1; PID:G;Genetics:
A;Gene: GDB:HLA-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: GDB:119310; OMIM:142800
A,Cross-references: GDB:119310; OMIM:142800
A,Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
E;1-24/Domain: signal sequence #stetuus predicted <SIG>
F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predi
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A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.
A;Reference number: 137120; MUID:92269955; PMID:1317015
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A;Reaidues: 1736 - RES>
A;Cross-references: UNIPROT:P01892; UNIPARC:UPI000016AD48; GB:M24042; NID:g187777; PIDN
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Pomain: immunoglobulin homology <IMM>
      A,Molecule type: mRNA
A,Realdues: 1-365 <REA
A;Cross-references: UNIPARC:UPIO00016AA63; EMBL:Z46633; NID:g575248; PIDN:CAA86602.1;
A;Note: submitted to the EMBL Data Library, November 1994
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C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                         C,Genetics:
A,Gene: hla-A
C,Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>
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Pred. No. 21;
4; Mismatches 2; Indels
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R;Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A;Title: Diversity and diversitication of HLA-A,B,C alleles.
A;Reference number: 136956; MUID:89235215; PMID:2715640
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Similarity 50.0%;
6; Conservative
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127 VGSDWRFLRGYH 138
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127 VGSDWRFLRGYH 138
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Matches 6; Conserv
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A;Residues: 1-519 <WIN>
A;Cross-references: UNIPROT:Q43246; UNIPARC:UPI0000126CF8; EMBL:U32579; NID:g987266; PID
A;Experimental source: strain B73
                                    probable sodium-translocating NADH dehydrogenase (ubiquinone) (EC 1.6.5.-) ngrB chain TC C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Bate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 A;Accession: B81690 B;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1466, 2000 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A;Accession: B81590
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q9PKB6; UNIPARC:UPI0000057982; GB:AE002323; GB:AE002160; NID A;Experimental source: strain Nigg (MoPn)
A;Genetics:
A;Gene: TC0550
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytochrome P450 DWARF3 - maize

cytochrome P450 DWARF3 - maize

N;Contains: oxidoreductase (EC 1.-.-.)

C;Species Zea mays (maize)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: T02263

E;WinkLer, R.G.; Helentjaris, T.

Plant Cell 7, 130-1317, 1995

A;Title: The maize dwarf3 gene encodes a cytochrome P450-mediated early step in gibberel

A;Reference number: Z14648; MUID:96004534; PMID:7549486

A;Accession: T02263

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 46.2%;
Matches 6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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82 VGGMWAFLRAF 92
                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-503 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: dwarf3
RESULT 14
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Search completed: May 19, 2006, 14:39:58 Job time : 14.2857 secs

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Sequence:

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Searched:

Database

Result

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Q56ys1 arabidopsis
Q4bfm2 burkholderi
Q2jit0 Cyanobacter
Q3m6c5 anabaena va
Q8x30 arabidopsis
Q9c5y2 arabidopsis
Q84zw0 pisum sativ
Q00857 fusarium sp
Q9c1b7 fusarium sp
Q5ch65 mus musculu
Q5gh67 rattus norv
Q5gh77 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                               de Kort C.A.D., Koopmanschap A.B.; "Nucleotide and deduced amino acid sequence of a cDNA clone encoding diapause protein 1, an amylphorin-type storage hexamer of the Colorado
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54; DB 2; Length 670;
Pred. No. 9.8;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              670 AA; 79825 MW; 8A000BA115BEC8A6 CRC64;
                                                                                                                                                                                                                                                                                                                                      Leptinotarsa decemlineata (Colorado potato beetle).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:006344; Floxygen transporter activity; IEA. GO; GO:0006810; P:transport; IEA. InterPro; IPR000966; Hemcoyanin. InterPro; IPR0005203; Hemcoyanin. C. InterPro; IPR005204; Hemcoyanin. C. InterPro; IPR005204; Hemcoyanin. N. PANTHER; PTHR11511; Hemcoyanin, 1. Pfam; PF00372; Hemcoyanin, 2: 1. Pfam; PF00372; Hemcoyanin, M; 1. Pfam; PF00372; Hemcoyanin, M; 1.
                                                                                                                                                                                                                                                                          Uni Prot KB/TrEMBL
                                                                                                                                                                                                                                                   670 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS, PRO0187, HAEMOCYANIN.
PROSITE, PRO0210, HEMOCYANIN_2; UNKNOWN_1.
          056781_ARATH
048FM2_BURNI
02JIT0_9CYAN
03MGCS_ANAVT
08XG08_RALSO
KAO2_ARATH
084ZW0_PEA
000857_FUSSP
09CH197_FUSSP
09CH197_FUSSP
05GH65_MOUSE
                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                 XKR6_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Insect Physiol. 40:527-535(1994)
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                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                       01-NOV-1996, integrated into Unit
01-NOV-1996, sequence version 1.
07-FBB-2006, entry version 25.
Diapause protein 1 (Fragment).
Name=Dp19;
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351 RKFYGALWSYLRHFFG 366
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                                                                                                                                                                                                                                                  Q25271 LEPDE PRELIMINARY;
Q25271;
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Matches 7; Conservative
3376
44006
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NCBI_TaxID=7539;
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Q3APYS CHLCH
ID Q3APYS_CHLCH
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SEQUENCE
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020xub5 godalia glo

020xub5 godalia glo

020xub5 godalia glo

030k79 paracoccus

059712 homo sapien

05918 pan troglod

05918 ratus norv

05948 synechocyst

04480 synechocyst

04480 synechocyst

04181 picrophium

0611t5 picrophium

0611t5 picrophilus

07642 caenorhabdi

03917 burkholderi

04184 burkholderi

03914 xenopus lae

05vm7 oryza sativ

09947 torque teno

049188 tetraodon n

05949 futurbipi
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rhizobium l
sodalis glo
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bordetella
bordetella
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144.247 Million cell updates/sec
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Q7w131
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            GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                  2849598 seqs, 925015592 residues
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Q3APYS_CHLCH
Q3APYS_CHLCH
Q94ZW1_PEA
Q97V7_RHILV
Q2NWBS_SODGL
Q7NWB3_GLOVI
Q2PK79_PANDE
XKR7_HÜMAN
XKR7_PANTR
XKR7_PANTR
XKR7_ROUSE
XKR7_ROUSE
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Q5AUSS_EMENI
Q5AUSS_EMENI
Q5AUSS_EMENI
Q5AUSS_EMENI
Q44QD1_CHLLI
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06L1T5_PICTO
0764A2_CABEL
039L57_BURS3
0456F4_9BURK
051K44_9BURK
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Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                         1 GLRRFIGSIWRFIRAFYG 18
                                                                                   May 19, 2006, 14:13:32
                                                                                                                                                                                                                                                                                                                                                     UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Match Length DB
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219
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Perfect score:
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NCBI_TaxID=387;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantãe, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Vicieae, Pisum.
                                                                                                                                                                                                                                                   US DOE JOINT GENOME [LARGE SCALE GENOMIC DNA].
US DOE Joint Genome Institute;
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Bryant D., Schmutz J., Larimer F., Land M., Kyrpides N., Ivanova N., Richardson P.;
"Complete sequence of Chlorobium chlorochromatii CaD3.";
Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22417727; PubMed=12529541; DOI=10.1104/pp.012963; Davidson S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.; The pea gene NA encodes ent-kaurenoic acid oxidase."; Plant Physiol. 131:335-34(12003).
                                                                                                                        Chlorobium chlorochromatii (strain CaD3).
Bacteria, Chlorobi, Chlorobia, Chlorobiales, Chlorobiaceae, Chlorobium/Pelodictyon group, Chlorobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.1%; Score 54; DB 2; Length 805; 53.8%; Pred. No. 12; cive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; CP000108; ABB28940.1; -; Genomic_DNA.
GG), GG:000524; F.ATP binding; IEA.
GG), GG:0004823; F.1eucine-tRNA ligase activity; IEA.
GG), GG:0016874; F.1igase activity; IEA.
GG), GG:0006429; P.1eucyl-tRNA aminoacylation; IEA.
Aminoacyl-tRNA synthetase; Complete proteome; Ligase.
SEQUENCE 805 AA; 92007 NW; A0C78BB3732AF54C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
-!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF537321, AAO23063.1; -; mRNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0020037; F:heme binding; IEA.
GO; GO:0005506; F:hron ion binding; IEA.
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:004497; F:menoxygenase activity; IEA.
                 22-NOV-2005, integrated into UniProtKB/TrEMBL 22-NOV-2005, sequence version 1.
21-FEB-2006, entry version 5.
LOUGH-LRNA synthetase class Ia (EC 6.1.1.4).
OrderedLocusNames=Cag_1688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003, integrated into UniProtKB/TrEMBL 01-JUN-2003, sequence version 1. 07-FBB-2006, entry version 21. Ent-kaurenoic acid oxidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pisum sativum (Garden pea).
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622 GISRFLGKVWRFV 634
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Best Local Similarity 53.8
Matches 7; Conservative
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Q84ZM1 PEA

10 Q84ZM1 PEA

C Q84ZM1;
DT 01-JUN-2003,
DT 01-JUN-2003,
DT 01-JUN-2004,
OS PLBM=EAOLIG
OS PRESULE
OS PRESULG
OS 
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ROS GO: 0016621; C:integral to membrane; IEA.

ROS GO: 0016621; C:integral to membrane; IEA.

ROS GO: 0016621; F:ATP binding; IEA.

ROS GO: 0016621; F:ATP ase activity; IEA.

ROS GO: 001665; F:ATPase activity; IEA.

ROS GO: 001665; F:ATPase activity; IEA.

ROS GO: 001665; F:protein transporter activity; IEA.

ROS GO: 0016503; F:protein transporter activity; IEA.

ROS GO: 0016508; F:protein transporter activity; IEA.

ROS GO: 0016508; P:protein transporter activity; IEA.

ROS GO: 0016508; P:protein transporter activity; IEA.

ROS GO: 0016508; P:protein transport.

ROS GO: 00166508; P:Protein transport.

ROS GO: 0016669; P:Protein transport.

ROS GO: 001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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"Analysis of the genetic region encoding a novel rhizobiocin from Rhizobium leguminosarum bv. viciae strain 305.";
Can. J. Microbiol. 47:495-502(2001).
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MEDLINE=21360352; Pubmed=11467725; DOI=10.1139/cjm-47-6-495;
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR00128; Cytochrome_P450.
InterPro; IPR002401; EP4501.
PANTHER; PTHR19393; Cytochrome_P450; 1.
Pfam; PF00067; P450; 2.
PRINTS; PR00463; EP450.
PROSITE; PR00086; CYTOCHROME_P450; UNKNOWN_1.
Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding; Monocoxygenaes; Oxidoreductase.
SEQUENCE 488 AA; 56478 MW; 503453CB6E43CB30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=rzcB;
Rhizobium leguminosarum bv. viciae.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.0%; Score 51; DB 2; 66.7%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001, integrated into UniProtKB/TrEMBL.
01-MAR-2001, sequence version 1.
07-FEB-2006, entry version 25.
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HSSP; P08716; 1MT0.
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PROSITE; PS50929; ABC_TMNIF; 1.
PROSITE; PS500211; ABC_TRANSPORTER 1; 1.
PROSITE; PS50893; ABC_TRANSPORTER 2; 1.
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SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 RHILV
QPF7V7 RHILV PRELIMINARY; PRT;
Q9F7V7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7
Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S FIGSIWRFIRAF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 FIGNMWSFLRAF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABC transporter RzcB.
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                49.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q3PK79 PARDE PRELIMINARY;
Q3PK79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 GLERFIRGYWRFI 116
DNA Res. 10:137-145(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GLRRFIGSIWRFI 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 69.2 tes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORFNames=PdenDRAFT 4722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
STRAIN=PD1222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                         Complete proteome. SEQUENCE 401 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARDE
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STRAIN=PCC 7421;
MEDLINR=22977040; PubMed=14621292; DOI=10.1093/dnares/10.4.137;
MRDLINR=22977040; PubMed=14621292; DOI=10.1093/dnares/10.4.137;
MRDLINR=22977040; PubMed=14621292; DOI=10.1093/dnares/10.4.137;
MARAMURA Y., Kaneko T., Sacto S., Mimuto M., Miyashita H., Tsuchiya T.,
Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of Gloeobacter violaceus PCC 7421, a
cyanobacterium that lacks thylakoids.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gloeobacter violaceus.
Bacteria; Cyanobacteria; Gloeobacteria; Gloeobacterales; Gloeobacter.
NCBI_TaxID=33072;
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            insights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Massive genome erosion and functional adaptations provide insight:
into the symbiotic lifestyle of Sodalis glossinidius in the tsetse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sodalis glossinidius str. 'morsitans'.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Toh H., Weiss B.L., Perkin S.A.H., Yamashita A., Oshima K.,
Hattori M., Aksoy S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 361;
                                                                            Length 735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                            4; Indels
  PS50990; PEPTIDASE C39; 1. 735 AA; 80717 MW; 0216259241F3630C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 AA; 40247 MW; 1257F70F3C3CA6EC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48; DB 2;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-2003, integrated into UniProtKB/TrEMBL. 15-DEC-2003, sequence version 1. 07-FEB-2006, entry version 13.
                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2006, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401 AA
                                                                                                                                                                                                                                                                                                                                                              361 AA
                                                                            51.0%; Score 50; DB 56.2%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP008232; BAE74260.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2, Mismatches
                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                      , sequence version 1.
                                                                                                                                                                                                               49.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative glycosyltransferase.
ORFNames=SG0985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 16:149-156(2006).
                                                                                                                                                                               1 GLRRFIGSIWRFIRAF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae; Sodalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gll1363 protein.
OrderedLocusNames=gll1363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 RFIGSIWRFIRAF 16
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                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 61.5
nes 8; Conservative
                                                  Query Match
Best Local Similarity
9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Morsitans;
                                                                                                                                                                                                                                                                                                                                                           OZNUBS SODGL
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       PROSITE;
                             SEQUENCE
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                                                                                                                                                                                                                                                                                                              RESULT 5
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Larimer F., Land M.;
"Annotation of the draft genome assembly of Paracoccus denitrificans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Paracoccus
dentirificans PD1222.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                   EMBL, BA000045; BAC89304.1; -; Genomic_DNA.
BioCyc; GVIO251221:GLiJ363-WONOMER; -.
GO; GO:0004040; F:amidase activity; IEA.
GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.
GO; GO:0009253; P:peptidoglycan catabolism; IEA.
InterPro; IPR002508; Amidase 3 hydro.
InterPro; IPR02901; Amidase 4.
Pfam; PF01520; Amidase 3, 1.
Pfam; PF01832; Glucosaminidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Paracoccus.
NCBI_TaxID=318586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48; DB 2; Length 401;
Pred. No. 52;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD1222.";
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 AA; 44051 MW; 903814BB688C170B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AAIT01000001; EAN68115.1; -; Genomic_DNA. GO; GO:0020037; F:heme binding; IEA. GO; GO:0005506; F:iron ion binding; IEA. GO; GO:0046872; F:metal ion binding; IEA. GO; GO:000497; F:metal ion binding; IEA. GO; GO:0006118; P:electron transport; IEA. InterPro; IPR001128; Cytochrome_P450. InterPro; IPR002401; EP4501. Pfam; PF00067; p450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2005, integrated into UniProtKB/TrEMBL 25-OCT-2005, sequence version 1. 07-FEB-2006, entry version 4.
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RESULT 9
XKR7 PANTR
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

A Deloukas P., Matchews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,

Deloukas P., Matchews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,

A Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

Bassley O.P., Bard C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

Ruck D., Burrill W.D., Butler A.P., Carder N.P.,

Clegg S., Cobley V.E., Collier R.E., Connor R.E., Carter N.P.,

Clegg S., Cobley V.E., Collier R.E., Connor R.E., Carter N.P.,

Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Clegg S., Cobley V.E., Collier R.E., Connor R.E., Carter N.P.,

Blington A.G., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

A Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

Huckle E., Hunt A.R., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RAY M.P., Kimberley A.M., Kinga A., Knights A., Laird G.K., Lawlor S.,

Lehvaeslaino M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

And Mine S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

A philimore B.J.C.T., Prathalingam S.R., Plunb R.W., Rangsy H.,

Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,

Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

Swann R.M., Sycamore N., Taylor R., Taylor R., Walliams S.A.,

Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Milming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R.,
                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential).
-!- SIMILARITY: Belongs to the XK family.
-!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
                                                                                                                                  ö
                                                                                                49.0%; Score 48; DB 2; Length 449; 80.0%; Pred. No. 59; 1; Indels ative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [MRNA].
Huang C.-H., Chen Y.;
"A superfamily of XK-related genes (XRG) widely expressed vertebrates and invertebrates.";
PRINTS; PR00463; EP4501.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
SEQUENCE 449 AA; 50659 MW; SF3EEC9E12AA3B35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                XXZ7 HUMAN STANDARD; PRT; 579 AA. QSGH72; Q9NUG5; 11-OCT-2005, integrated into UniProtXB/Swiss-Prot. 01-MAR-2005, entry version 1. 07-FEB-2006, entry version 8. XK-related protein 7. Name=XKR7; Synonyms=C20orf159, XRG7;
                                                                                                                                    8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       414:865-871 (2001)
                                                                                                                                                                   7 GSIWRFIRAF 16
                                                                                                                                                                                                  13 GSVWRFIRDF 22
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-0CT-2005, integrated into UniProtKB/Bwiss-Prot.
13-SEP-2005, sequence version 1.
07-FEB-2006, entry version 6.
XK-related protein 7.
Name-XKR7; Synonyms-XRG7;
Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Ptimates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 77;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang C.-H., Chen Y.;
"A superfamily of XK-related genes (XRG) widely expressed vertebrates and invertebrates.";
Submitteed (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                        Score 48; DB 1; Length 579;
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
6DFE1191093E85D4 CRC64;
                                                                                                                                                                                                                        D8D0FF64B9EDD53D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XK-related protein 7./FTId=PRO_0000190790.
                                                                              XK-related protein 7
EMBL, AY534245; AAT07094.1; -; mRNA.
EMBL; AL031658; CAB88102.1; ALT_SEQ; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   579 AA.
                                                                                                                                                                                                                                                                                         4; Mismatches
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Potential.
Potential.
Potential.
                            Ensembl; ENSG0000101321; Homo sapiena.
HGNC; HGNC:23062; XKR7.
Membrane; Transmembrane.
                                                                                                            Potential.
Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                          63826 MW;
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190 LGQVWRYLRALY 201
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190 LGQVWRYLRALY 201
                                                                                                                                                                                                                                                                                         6, Conservative
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les 6; Conservative
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260 2
314 3
355 3
384 4
415 4
                                                                                                                                                                                                                          579 AA;
                                                                                                                                                                                                                                                                     Local Similarity
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Q49LS1;
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                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
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Huang C.-H., Chen Y.;
Huang C.-H., Chen Y.;
A superfamily of XX-related genes (XRG) widely expressed in vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-: SUBCELLUIAR LOCATION: Membrane; multi-pass membrane protein
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                                                                                                                           11-OCT-2005, integrated into UniProtKB/Swiss-Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XK-related protein 7
/FTId=PRO_0000190789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB 1;
Pred. No. 77;
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                                                                                     580 AA
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Ensembl; ENSMUSG0000042631; Mus musculus.
MGI; MGI:3526711; Xkr7.
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                                                                                       PRT;
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07-FBB-2006, entry version 8.
XK-related protein 7.
Name=Xkr7; Synonyms=Xrg7;
                                                                                                                                                  01-MAR-2005, sequence version 1. 07-FBB-2006, entry version 10. NK-related protein 7. Name=Kkr7; Synonyms-Xrg7; Mus musculus (Mouse).
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190 LGQVWRYLRALY 201
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                                                                                       STANDARD;
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Huang C.-H., Chen Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580 AA;
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                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Potential).
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                                                                                       XKR7 MOUSE
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Membrane;
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QSGHS6;
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                                                                                                         Q5GH64;
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                                                                   XKR7_MOUSE
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Distributed under the Creative Commons Attribution-NoDerivs License
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Batzoglou S., Lee S.-I., Bastuerkmen M., Spevak C.C., Clutterbuck J.,
Kapitonov V., Jurka J., Scazzocchio C., Farman M., Butler J.,
Burchil S., Harita S., Braus G.H., Draht O., Busch S., D'Enfert C.,
Bouchier C., Goldman G.H., Dell.Pedersen D., Griffiths-Jones S.,
Doonan J.H., Yu J., Vienken K., Pain A., Freitag M., Selker E.U.,
Archer D.B., Penalva M.A., Oakley B.R., Momany M., Tanaka T.,
Kumagai T., Asai K., Machida M., Nierman W.C., Denning D.W.,
Caddick M., Hynes M., Paoletti M., Fischer R., Miller B.L., Dyer P.S.,
Sachs M.S., Osmani S.A., Birren B.W.;
Sequencing of Aspergillus nidulans and comparative analysis with A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                   vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
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Eurotiales, Trichocomaceae, Emericella.
superfamily of XK-related genes (XRG) widely expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 1; Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        8F4907F391B4F5BE CRC64;
                                                                                                                                                                                                                  XX-related protein 7./FTId=PRO_0000190791.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-APR-2005, integrated into UniProtKB/TrEMBL 26-APR-2005, sequence version 1. 07-MAR-2006, entry version 6. Hypothetical protein. ORFNames=AN7955.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  597 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 77;
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PubMed=16372000; DOI=10.1038/nature04341;
                                                                        (Potential).
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QSAUSS;
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580 AA;
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GO; GO:0016020; C:membrane; IEA. GO; GO:0015205; F:nucleobase transporter activity; IEA.

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STRAIN-DSM 245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDLINE-97061201; PubMed=8905231; DOI=10.1093/dnares/3.3.109;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                        Gaps
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GO; GO:0015931; P:nucleobase, nucleoside, nucleotide and nucl.
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13-SEP-2005, sequence version 1.
21-FEB-2006, entry version 9.
21-FEB-2006, entry version 9.
CHOSTANA synthetase bacterial/mitochondrial, class Ia.
CRFNames=ClimDRAFT 1980;
Chlorobi, Chlorobi, Chlorobia, Chlorobiales, Chlorobiaceae, Chlorobium/Pelodictyon group, Chlorobium.
                                                                                                      In 49.0%; Score 48; DB 2; Length 597; Similarity 47.1%; Pred. No. 79; 8; Conservative 5; Mismatches .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.0%; Score 48; DB 2; Length 627; 38.9%; Pred. No. 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                    InterPro, IPR001248; Cyt_pur_permease.
Pfam, PF02133; Transp_Cyt_pur; 1.
Hypothetical protein.
SEQUENCE 597 AA; 65089 MW; E686F4978F37BF5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    627 AA; 69725 MW; BBE187A53BF96229 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OrderediocusNames=s111858;
Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1997, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           805 AA.
                                                                                                                                                                                                                                                                                                                                                                        627 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BA000022; BAA18591.1; -; Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      P74489 SYNY3 PRELIMINARY; PRT;
P74489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S76462; S76462.
BioCyc; SSP1148:SLL1858-MONOMER; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997, sequence version 1. 07-FEB-2006, entry version 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  597 GLEQLLGKIWQWLRQKFG 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GLRRFIGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                             159 LRSFVGCMWFGMQAFWG 175
                                                                                                                                                                                                                    2 LRRFIGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q44QD1_CHLLI PRELIMINARY;
Q44QD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 38.9 tes 7; Conservative
                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=290315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
SEQUENCE 627 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sll1858 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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0440D1 CHI
0440D AC
0440C
DT 13-SE
DT 13-SE
DT 13-SE
DT CHI
05 CHI
06 CHI
07 CHI
08 CHI
08 CHI
08 CHI
08 CHI
08 CHI
08 CHI
09 CHI
09
                                                                                                                                                                                                                                                                                                                               RESULT 13
P74489 SY
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US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Chlorobium limicola DSM 245.";
                                                                                                                                                                                                                                                                                                 US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Chlorobium limicola DSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=DSM 266;
US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Chlorobium
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!-CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Chlorobium/Pelodictyon group; Chlorobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 48; DB 2; Length 805;
Pred. No. 1.18+02;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2005, integrated into UniProtKB/TrEMBL.
13-SEP-2005, sequence version 1.
13-SEP-2006, entry version 9.
1eucyl-TRNA synthetase bacterial/mitochondrial, class Ia.
ORFNames-Cphaz66DRAFT 2546;
Chlorobium phaeobacteroides DSM 266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phaeobacteroides DSM 266.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phaeobacteroides DSM 266.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AAHJO1000009; EAW43320.1; -; Genomic_DNA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000423; F:leucine-tRNA ligase activity; IEA.
GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
InterPro; IPR002302; Leu tRNAsyn_la.
PRINTS; PR00331; tRNA-synt_l; 1.
PRINTS; PR00985; TRNASYNTHLEU.
TIGRPAM; TIGR00395; leus_bact; 1.
Aminoacyl-tRNA synthetase.
SEQUENCE 805 AA; 91997 MW; D4F3FE28F9B92DF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
STRAIN=DSM 266;
SITAIN=DSM 266;
Larimer F., Land M.;
"Annotation of the draft genome assembly of Chlorobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        816 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 49.0%;
Local Similarity 46.2%;
es 6; Conservative
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Q43K01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |: ||:| :|| :
622 GISRFLGKVWRLV 634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                     [2]
NUCLEOTIDE SEQUENCE.
STRAIN=DSM 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=290317;
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CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms CC Distributed under the Creative Commons Attribution-NoDerive License CC Distributed under the Creative Commons Attribution-NoDerive License CC COPYRIGHTED UNDER CO. GO:000524; F:ATP binding; IEA.

DR GO; GO:000423; F:leucine-tRNA ligase activity; IEA.

DR GO; GO:000423; F:leucy-tRNA aminoacylation; IEA.

DR GO; GO:000423; F:leucy-tRNA mainoacylation; IEA.

DR GO; GO:000423; F:leucy-tRNA mainoacylation; IEA.

DR PRINTS; PRO0313; tRNA-synt_1; 1.

DR PRINTS; PRO0395; TRNASYNTHLEU.

DR PRINTS; PRO0395; TRNASYNTHLEU.

DR PRINTS; PRO0395; TRNASYNTHLEU.

CO SEQUENCE 816 AA; 93335 WW; 6770B1DAC50560F1 CRC64;

Aminoacyl-tRNA synthetase.

SC SEQUENCE 816 AA; 93335 WW; 6770B1DAC50560F1 CRC64;

Aminoacyl-tRNA synthetase.

SO SEQUENCE 816 AA; 93335 WW; 6770B1DAC50560F1 CRC64;

Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps
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Search completed: May 19, 2006, 14:38:14 Job time: 115.429 secs

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RESULT 1
US-08-940-095-242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                    (without alignments)
63.384 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / EMC_Celerra_SIDS3/ptodata/2/jaa/5_COMB.pep:*/
/EMC_Celerra_SIDS3/ptodata/2/jaa/6_COMB.pep:*/
/EMC_Celerra_SIDS3/ptodata/2/jaa/7_COMB.pep:*/
/EMC_Celerra_SIDS3/ptodata/2/jaa/HCOMB.pep:*/
/EMC_Celerra_SIDS3/ptodata/2/jaa/PCTUS_COMB.pep:*/
/EMC_Celerra_SIDS3/ptodata/2/jaa/RE_COMB.pep:*/
/EMC_Celerra_SIDS3/ptodata/2/jaa/RE_COMB.pep:*/
/EMC_Celerra_SIDS3/ptodata/2/jaa/RE_COMB.pep:*/
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                                                                                                                                           ; Search time 24.8571 Seconds
GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-08-940-093-242
US-08-940-096-242
US-09-465-719-242
US-09-453-605-242
US-09-453-841-242
US-09-453-841-242
US-09-453-841-242
US-09-453-840-242
US-09-453-840-242
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US-09-453-840-242
US-09-465-118-242
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US-09-465-118-242
US-09-465-1190-3
US-08-488-379-3
US-08-488-379-3
US-08-475-399A-3
US-08-475-399A-3
US-08-475-399A-3
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US-08-475-399A-2
US-08-475-399A-2
US-08-475-399A-2
US-08-475-399A-2
US-08-475-399A-2
US-08-480-190-2
US-08-480-190-2
US-08-480-190-2
US-08-480-190-2
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US-08-480-190-2
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                                                                                                                                                                                                                                                                                                                                                                                                        650591 seqs, 87530628 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                      1 GLRRFIGSIWRFIRAFYG 18
                                                                                                                                             May 19, 2006, 14:38:42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                         US-10-712-447-115
98
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
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T-US93-07545 08-480-190-108-480-190-108-488-379-6.08-475-399A-6.08-077-255A-108-127-954-11-08-127-954-1	US-08-12/-954-144
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7 0 0 0 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1	45

## ALIGNMENTS

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Sequence 242, Application US/08940095
Patent No. 6004925
Patent No. 6004926
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RESULT 4
US-09-465-719-242
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                                                                                                                                          Sequence 242, Application US/08940093
; Sequence 242, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
    APPLICANT: Dasseux, Jean-Louis
    APPLICANT: Sekul, Renate
    APPLICANT: Buttner, Klaus
    APPLICANT: Metz, Gunther
    TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
    CORRESPONDENCE: 258
    CORRESPONDENCE: 258
    CORRESPONDENCE: 258
    CORRESPONDENCE ADDRESS:
    STREET: 1155 Avenue of the Americas
    CITY: New York
                                               Gaps
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Query Match 75.5%; Score 74; DB 2; Length 18; Best Local Similarity 61.1%; Pred. No. 3.9e-05; Matches 11; Conservative 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDUNT TYEE DISKETCE
COMPUTER: IBM Compatible
SOFFWARE: FESTERO, Version 2.0
SOFFWARE: FESTERO, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,093
FILING DATE: 29-5EP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORWATION:
NAME: COTTACT, LAURER:
ATTORNEY/AGENT INFORWATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 651-493-556
TELEFAX: 6614 PENNIE
TELEFAX: 6614 PENNIE
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                        1 GLRRFIGSIWRFIRAFYG 18
|:::|:||||:||
1 GIKKFLGSIWKFIKAFVG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 61.19
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
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RESULT 3
US-08-940-096-242
Sequence 242, Application US/08940096
Patent No. 6046166
GENERAL INFORMATION:

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Sequence 242, Application US/09465719

Patent No. 6265377

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Matther, Klaus
APPLICANT: Matther, Klaus
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
MUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
              APPLICANT: Sekul, Renate
APPLICANT: Butiner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
WUMBER OF SEQUENCES: 228
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.5%; Score 74; DB 2; Length 18; 61.1%; Pred. No. 3.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0005-999
TELECOMMUNICATION INFORMATION:
TELEPAN: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
                                                                                                                                                                                                                                                                                                COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
CLASSIFICATION DATA:
APPLICATION WHERE:
APPLICATION WHERE:
APPLICATION WHERE:
ALFLING DATE:
APPLICATION WHERE:
                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
Dasseux, Jean-Louis
Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GLRRFIGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: No. 6046166e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10036-2811
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Suture, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Dufourcq, Jean
APPLICANT: Dufourcq, Jean
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
TITLE OF INVENTION: APPLIPOPROTEIN A-1 AGONISTS
TITLE OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                             Score 74; DB 2; Length 18;
Pred. No. 3.9e-05;
6; Mismatches 1; Indels
                    009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIPECATION
PAINE APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUKA A
REGISTRATION NUMBER: 30,742
REPERNICE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: NO. 6329341e

SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-453-605-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSEE: Pennie & Edmonds LLP
T: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESEQ VESTION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-453-838-242; Sequence 242, Application US/09453838 patent to 6376464; GENERAL INFORMATION:
                  REFERENCE/DOCKET NUMBER:
TELLECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 650-493-5556
                                                                                                     INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GLRRFIGSIWRFIRAFYG 18
                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: No. 6376464e
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 660-493-5556
TELEFAX: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
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Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.5%; Score 74; DB 2; Length 18; 61.1%; Pred. No. 3.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                     APPLICATION:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 29-SEP-197
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NIFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAK: 660-491-4935
TELERAK: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FEBLESO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,605
FILING DATE: 26-No. 6329341-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ 'Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 242, Application US/09453605
Patent No. 6329341
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6265377e
US-09-465-719-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 61.1;
Matches 11; Conservative
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Sequence 242, Application US/09453841
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US-09-453-833-242
                          Patent No. 6573
                                                                                                                                                                                                                                                                                                                                                                STATE: N
COUNTRY:
ZIP: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
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                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klauus
APPLICANT: Cornut, Isabelle
APPLICANT: Ornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufcourcq, Jean
TITLE OF INVENTION: GENE THERAPY APPROACHES TO
TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

NUMBER OF SEQUENCES: 274
ADDRESSEE: Pennie & Edmonds LLP
                                                                                            ö
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                                            Score 74; DB 2; Length 18;
Pred. No. 3.9e-05;
                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,136
FILING DATE: 29-SEP-1997
CLASSIFICATION NUMBER: 05/08/940,136
FILING DATE: 10-NTORWATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0007-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEG 1D NO: 242:
TELEFA: 650-493-556
TELECOMMUNICATION INFORMATION FOR SEQ 1D NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acid
STRAMDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No: 6518412e
US-08-940-136-242
                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                           Sequence 242, Application US/08940136
Patent No. 6518412
GENERAL INFORMATION:
                                                                                                                                                                1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GLRRFIGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:::|:|||:||:|| | GIKKFLGSIWKFIKAFVG 18
                                                                                                                                      1 GLRRFIGSIWRFIRAFYG 18
                                               75.5%;
                                            Query Match
Best Local Similarity 61.1
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
  US-09-453-838-242
                                                                                                                                                                                                                                                                             JS-08-940-136-242
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Sequence 242, Application US/09453833

Sequence 242, Application US/09453833

Patent No. 6602854

GENERAL INFORMATION:
APPLICANT: Baseaux, Jean-Louis
APPLICANT: Bettner, Klaus
APPLICANT: Gornut, Isabelle
APPLICANT: Buttner, Gunther
APPLICANT: Difourcq, Jean
TITLE OF INVENTION: APOLIPOROTEIN A-1 AGONISTS
TITLE OF INVENTION: APOLIPOROTEIN A-1 AGONISTS
TITLE OF INVENTION: APOLIPOROTEIN A-1 AGONISTS
MUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
GENERAL INFORMATION:
APPLICANT: Desseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Difourcq, Jean
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FRAELSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,841
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION
APPLICATION NUMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 00915
TELECOMMUNICATION INFORMATION:
TELEFAX: 650-493-4935
TELEFAX: 66141 PENNIE
INFORMATION FOR SEO IN 00: 242: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GLRRFIGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                        ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FAST FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: No. 6573239e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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RESULT 8 US-09-453-841-242

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009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,840
FILING DATE:
CLASSPICATION:
PRIOR APPLICATION
APPLICATION NUMBER: 08/940,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSE: Pennie & Edmonds LLP
1: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 242, Application US/09453840
Patent No. 6716816
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LBUTA A
REGISTRATION NUMBER: 30,742
REFERENCE/POCKET NUMBER: 0091:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GLRRFIGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6630450e
US-09-453-826-242
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 61.1;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & STREET: 1155 Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-453-840-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: N
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| Sequence 242, Application US/09453826
| Patent No. 6630450
| GENERAL INFORMATION:
| APPLICANT: Dasseux, Jean-Louis APPLICANT: Buttner, Klaus APPLICANT: Genul, Isabelle APPLICANT: Cornut, Isabelle APPLICANT: Dufourcq, Jean TITLE OF INVENTION: APOLIPOPROTEIN A-I ACONISTS TITLE OF INVENTION: APOLIPOPROTEIN A-I ACONISTS TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS NUMBER OF SEQUENCES: 258
| CORRESPONDENCE ADDRESS: | ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas CITY: New York CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.96-05;
                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECPHONE: 650-493-4935
TELEPAX: 650-493-5556
TELEPAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 75.5%; Score 74; DB Best Local Similarity 61.1%; Pred. No. 3.9e Matches 11; Conservative 6; Mismatches
STREET: 1155 Avenue of the Americas CITY: New York
                                                    COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESSES Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOSS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,826
CLASSIFICATION:
                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:::|:||||:|| |
1 GIKKFLGSIWKFIKAFVG 18
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// MOLECULE TYPE: No. 6602854e

US-09-453-833-242
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Mctz, Gunther
APPLICANT: Mctz, Gunther
APPLICANT: Difourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
NUMBER OF SEQUENCES: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.5%; Score 74; DB 2; Length 18; 61.1%; Pred. No. 3.9e-05; Live 6; Mismatches 1; Indels
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAUKA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-5556
TELEPAX: 66149 FENNIE
TELEPAX: 66149 FENNIE
TELEPAX: 66149 FENNIE
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
LENGTH: 12 amino acids
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RESULT 14
US-10-283-599-242
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Cornut, Isabelle
Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
                                                                                                                                                                      Gaps
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                                                                                                                       Query Match 75.5%; Score 74; DB 2; Length 18; Best Local Similarity 61.1%; Pred. No. 3.9e-05; Matches 11; Conservative 6; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNATE: NA
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUUT TYPE: Diskette
COMPUTER: DEN Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, LAURE A
REGISTRATION NUMBER: 30,742
REFERENCE/COCKET NUMBER: 009196-0006-999
TELEPHONE: 650-493-4935
TELEFRAX: 65141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds Lip
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: No. 6734169e
SEQUENCE DESCRIPTION: SEQ ID NO: 242:
                                                                                                                                                                                                                                                                                                                                                               Sequence 242, Application US/09865989
Patent No. 6734169
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 18 amino acids
                                                                                                                                                                                                                                        1 GIKKFLGSIWKFIKAFVG 18
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STRANDEDNESS: single
         STRANDESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6716816e
US-09-453-840-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sekul, Renate
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                         RESULT 12
US-09-865-989-242
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APPLICANT: British Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS: 2
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 242, Application US/10283599

Batent No. 6844327

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Buttner, Klaus

APPLICANT: Cornut, Isabelle

APPLICANT: Outcher

APPLICANT: Dufourcq, Jean

APPLICANT: Such PREAPY APPROACHES TO

TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-1 AGONISTS AND THBIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.5%; Score 74; DB 2; Length 18; 61.1%; Pred No. 3.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,834
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 009196-0004-999
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
Sequence 242, Application US/09453834 Patent No. 6753313
                                               GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GLRRFIGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                   STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPAIDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: No. 6753313e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 11; Conservative
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Query Match 75.5%; Score 74; DB 2; 1
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1;
                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 09196-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHORE: 650-493-4935
TELEFRA: 650-493-556
TELERA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                  FILING DATE: 17-Dec-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
APPLICATION NUMBER:
APPLICATION NUMBER: US/09/465,718
FILING DATE: 17-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: May 19, 2006, 14:42:55 Job time : 24.8571 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GLRRFIGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: No. 6900177e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-465-718-242
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| Sequence 242, Application US/09465718
| Patent No. 6900177|
| GENERAL INFORMATION:
| APPLICANT: Buttner, Klaus
| APPLICANT: Buttner, Klaus
| APPLICANT: Manual APPLICANT: Buttner, Cornut, Isabelle
| APPLICANT: Manual APPLICANT: New York
| CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        009196-0007-999
                                                                                                                                                             COUNTY.

COUNTY.

COUNTY.

ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DISKETTE
COMPUTER: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: PASTEM: DOS
SOFTWARE: PASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,599
FILING DATE: 29-CCT-2002
CLASSIFICATION DATA:
APPLICATION NUMBER: US/40,136
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COCLZZi, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TEMMINICATION: SEQUENCE:
SEQUENCE CHARACTERISTICS:
                                 STREET: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURREMY APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GIKKFLGSIWKFIKAFVG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6844327e
US-10-283-599-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 18 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
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Gaps

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Length 18; ;; 1; Indels

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Appl Appl 7, Appl 9, Appl 0, Appl 14, Appl 100, Appl 41, Appl

OM protein

Run on:

Sequence:

Searched:

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Sequence 115, Application US/10712447

| Sequence 115, Application US/10712447
| Publication No. US20040186057A1
| GENERAL INFORMATION:
| APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
| APPLICANT: DATTA, GEETA
| TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
| TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
| TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
| TITLE OF INVENTION: 2003-11-13
| FILE REFERENCE: 112739-123US
| CURRENT PELING DATE: 2003-11-13
| PRIOR FILING DATE: 2003-11-13
| NUMBER OF SEQ ID NOS: 210
| SOFTWARE: Patentin Ver. 3.2
| SEQ ID NOS: 210
| SEQ ID NOS: 210
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US-10-712-447-116

Sequence 116, Application US/10712447

Sequence 116, Application US/10712447

Sequence 116, Application No. US20040186057A1

GENERAL INFORMATION:
MAPPLICANT: ANNUTHARAMIAH, GATTADAHALLI M.
MAPLICANT: GARBER, DAVID W.
MAPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APPLIFORPORFOTEIN E AND METHODS OF USE
TITLE OF INVENTION: UNMBER: US/10/712,447

CURRENT APPLICATION NUMBER: US/10/712,447

PRIOR FILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence ?
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                       Sequence
Sequence
Sequence
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                                                                                                       Sequence
                                                                                                                                                                                                                               Sequence
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                                                                             Sequence
                     Sequence
                                                       Sequence
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US-10-712-447-22
US-10-712-447-78
US-10-712-447-120
US-10-712-447-130
US-10-712-447-130
US-10-712-447-58
US-10-712-447-58
US-10-712-447-77
US-10-712-447-94
US-10-712-447-94
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US-10-712-447-97
US-10-712-447-97
US-10-712-447-97
US-10-712-447-97
US-10-712-447-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
COTHER INFORMATION:
US-10-712-447-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-712-447-115
       Query Match
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10, Appli
11, Appl
117, App
117, App
117, App
117, Appl
21, Appl
21, Appl
23, Appl
4, Appl
112, Appl
99, Appl
113, Appl
113, Appl
113, Appl
113, Appl
114, Appl
117, Appl
117, Appl
118, Appl
117, Appl
118, Appl
119, Appl
111, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                                                                                                                                                                                                               (without alignments)
102.575 Million cell updates/sec
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Sequence 2
Sequence 2
Sequence 3
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                                                                                                                                                                                  May 19, 2006, 15:18:19 ; Search time 81.2857 Seconds
                               GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-712-447-8
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US-10-712-447-10
US-10-712-447-13
US-10-712-447-13
US-10-712-447-131
US-10-712-447-131
US-10-712-447-91
US-10-712-447-91
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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98
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Maximum DB seq length: 2000000000
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Perfect score:
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Result No.

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Gaps

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Sequence 8, Application US/10712447
Publication No. US20040186057A1
GENERAL INFORMATION:
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                                                                                    ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9%;
Matches 16; Conservative
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 5
LENGTH: 18
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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 10
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US-10-712-447-8
                                                                  TYPE: PRT
                                                                                                        FEATURE:
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US-10-712-447-5

Squence 5, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TURENT APPLICATION NUMBER: US/10/712,447

CURRENT APPLICATION NUMBER: G0/425,821

PRIOR PILING DATE: 2002-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:
APPLICANT: GARBER DAVID W.
APPLICANT: DATTA, GETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND
FILE REFERENCE: 112739-123US

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

PRIOR FILING DATE: 2003-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENTIN VET. 3.2

LENGTH: 18
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                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide
US-10-712-447-116
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100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 95.9%; Score 94; DB 4; Length 18; Best Local Similarity 88.9%; Pred. No. 4.7e-07; Matches 16: Conservative 2; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
  NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 116
LENGTH: 18
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APPLICANT: ANATHARAMIAH, GATTADAHALLI M.
APPLICANT: GARBER, DAVID W.
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APPLICANTION: APPLICANTION APPLICANTION NUMBER: US/10/712,447
CURRENT FILING DATE: 2003-11-13
PRIOR PILING DATE: 2002-11-13
PRIOR PILING DATE: 2002-11-13
SOFTWARE: PATENTIN UNER: 60/425,821
PRIOR FILING DATE: 2002-11-13
SOFTWARE: PATENTIN VOY: 3.2
SEQ ID NO 8:
LENGTH: 18
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| Sequence 10, Application US/10712447
| Sequence 10, Application US/10712447
| Publication No. US20040186057A1
| GENERAL INFORMATION:
| APPLICANT: ANATHARAMIAH, GATTADAHALLI M.
| APPLICANT: GARBER, DAVID W.
| APPLICANT: GARBER, DAVID W.
| APPLICANT: GARBER, DAVID W.
| TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
| TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
| FILE REFERENCE: 112739-122US
| CURRENT APPLICATION NUMBER: US/10/712,447
| PRIOR FILING DATE: 2003-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: peptide US-10-712-447-5
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US-10-712-447-8
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                                                                                                                                 Query Match

95.9%; Score 94; DB 4; I
Best Local Similarity 88.9%; Pred. No. 4.7e-07;
Matches 16; Conservative 2; Mismatches 0;
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Pred. No. 4.7e-07;
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RESULT 9
US-10-712-447-127
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Sequence 117, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: BANTHARAMIAH, GATTADAHALLI M.

APPLICANT: BANTHARAMIAH, GATTADAHALLI M.

APPLICANT: BATTA, GEETA

TITLE OF INVENTION: APOLIPOROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOROTEIN E AND METHODS OF USE

FILE REFERENCE: 112739-11230

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

FRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENTIN Ver. 3.2

SEQ ID NO 117
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Sequence 13, Application US/10712447

Sequence 13, Application US/1071247

Publication US/20040186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

FILE REPERENCE: 112739-12305

CURRENT FILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

PRIOR FILING DATE: 2002-11-13

SEQ ID NO 13

LENGTH: 18

TYPE: PRT

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TYPE: PRT

REGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
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                                                                                                                                                                                                                                                                                                Query Match 95.9%; Score 94; DB 4; Length 18; Best Local Similarity 88.9%; Pred. No. 4.7e-07; Matches 16; Conservative 2; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
FEATURE:
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Sequence 127, Application US/10712447

| Bublication No. US20040186057A1
| GENERAL INFORMATION:
| APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
| APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
| APPLICANT: DATTA, GEETA
| TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
| TITLE OF INVENTION: APPLICATION SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
| TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
| TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
| TITLE OF INVENTION NUMBER: US/10/712,447
| CURRENT APPLICATION NUMBER: 60/425,821
| PRIOR FILING DATE: 2003-11-13
| MUMBER OF SEQ ID NOS: 210
| SOFTWARE: PATENT UVET: 3.2
| SEQ ID NO 127
| LENGTH: 18
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; Bublication No. US20040186057A1
; Fublication No. US20040186057A1
; GENERAL INFORMATION:
    APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; TITLE OF INVENTION NUMBER: US/10/712,447
; CURRENT APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PALENTIN Ver. 3.2
; SEQ ID NO 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide
US-10-712-447-127
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: peptide US-10-712-447-117
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                                                                                                                    95.9%; Score 94; DB 4; Length 18;
88.9%; Pred. No. 4.7e-07;
tive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                          Query Match
Best Local Similarity 88.9°
Matches 16; Conservative
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Gaps

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Indels

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US-10-712-447-21

Sequence 21, Application US/10712447

Publication No. US20040186057A1

Sequence 21, Application US/10712447

Publication No. US20040186057A1

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: APPLICANT: GARBER, DAVID W.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLICADOR

FILE REFERENCE: 112.739-12.346

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT PILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

FRIOR FILING DATE: 2002-11-13

SOFTWARE: PATENTIN US: 210

SEQ ID NO 21

LENGTH: 18
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US-20-0-712-447-53

Sequence 53, Application US/10712447

Sequence 53, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

FILE REFERENCE: 112739-12308

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 88; DB 4; Length 18; Pred. No. 3.7e-06;
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  Mismatches
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PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 53
LENGTH: 18
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LOCATION: (3)—
OTHER INFORMATION: (DiMe) Lys
PEATURE:
NAME/KEY: MOD RES
LOCATION: (14)
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Best Local Similarity 77.8%;
Matches 14; Conservative
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  14; Conservative
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Sequence 91, Application US/10712447

Fublication Vo. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: ARBRER, DAVID W.

TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES

CURRENT PILION DAPOLIPOPROTEIN B AND METHODS OF USE

CURRENT FILING DATE: 2003-11-13

PRIOR PILING DATE: 2003-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PALENTIN VOR. 3.2

SEQ ID NO 91

LENGTH: 18
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Sequence 129, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHARMIAH, GATTADAHALLI M.

APPLICANT: DATPA, GEETA

APPLICANT: DATPA, GEETA

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND

FILE REPRENCE: 112799-123US

CURRENT APPLICATION NUMBER: US/10/712,447

PRIOR FILING DATE: 2003-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PARENTIN VEV. 3.2

SEQ ID NO 129

LENGTH: 18
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US-10-712-447-129
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                         Score 94; DB 4; Length 18;
Pred. No. 4.7e-07;
2; Mismatches 0; Indels
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                         Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity
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US-10-712-447-129
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US-10-712-447-74

i Sequence 74, Application US/10712447

i Publication No. US20040186057A1

i GENERAL INFORMATION:
    PAPLICANT: ANATHRARMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APPLICANTON: APPLICANTON: APPLICANTON: APPLICANTON: APPLICANTON: APPLICANTON: APPLICANTON: APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

PRIOR FILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

SOFTWARE: PATENTIN VOIS: 210

SOFTWARE: PATENTIN VOIS: 3.2

SEQ ID NO 74

LENGTH: 18

TUBENCH: 18
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ORGANISM: Artificial Sequence
FEATURE:
FOHER INFORMATION: Description of Artificial Sequence: Synthetic
JOTHER INFORMATION: peptide
US-10-712-447-74
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89.8%; Score 88; DB 4; Length 18;
Best Local Similarity 77.8%; Pred. No. 3.7e-06;
Matches 14; Conservative 4; Mismatches 0; Indels
                                                                   Score 88; DB 4; Length 18;
Pred. No. 3.7e-06;
4; Mismatches 0; Indels
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Best Local Similarity 77.8%;
Matches 14; Conservative
; OTHER INFORMATION: (Dime)Lys US-10-712-447-53
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Search completed: May 19, 2006, 15:27:57 Job time : 81.2857 secs

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88, Appl
2, Appli
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569, App
23, Appl
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VIG-09-949-925-111

Sequence 111, Application US/0994925

PUBLICANT NO. US20060099575A9

GENERAL INFORMATION:

TITLE OF INVANITION:

FILE REPRENCE: P20.3P2

CURRENT FILING DATE: 2001-09-12

CURRENT FILING DATE: 2000-12-09

PRIOR APPLICATION NUMBER: US 60/232,150

PRIOR APPLICATION NUMBER: US 60/073,160

PRIOR FILING DATE: 1998-01-37

PRIOR FILING DATE: 1998-01-30

PRIOR FILING DATE: 1998-01-30

PRIOR PILING DATE: 1998-01-30
US-11-190-750-137

US-11-204-427-1

US-11-204-427-1

US-10-488-015-17

US-10-505-928-859

US-11-249-111-88

US-11-249-111-88

US-11-221-738-6

US-11-221-738-6

US-11-280-997-1

US-11-280-997-2

US-11-280-997-2

US-11-280-997-25

US-11-280-997-25
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US-09-949-925-111
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ORGANISM: Homo sapiens
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NAME/KEY: SITE
     LOCATION:
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Sequence 2947, Ap
Sequence 142, App
Sequence 543, App
Sequence 5, Appli
Sequence 109, Appli
Sequence 115, Appli
Sequence 115, Appli
Sequence 48, Appli
Sequence 40, Appli
Sequence 40, Appli
Sequence 18, Appli
Sequence 16, Appli
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/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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                                                                                                                            May 19, 2006, 15:18:37 ; Search time 2.14286 Seconds (without alignments) 17.943 Million cell updates/sec
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                      GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-511-937-2401

US-10-505-928-142

US-10-505-928-543

US-11-169-140-109

US-11-109-140-109

US-11-242-505A-48

US-11-204-427-784-87

US-11-204-427-784-87

US-11-304-129-40

US-11-304-129-40

US-11-342-505A-18

US-11-342-505A-18

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US-10-196-749-336
US-11-024-544A-169
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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ORGANISM: Homo sapiens

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PRIOR FILING DATE: 2003-04-24

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 3117

SOFTWARE: Patentin Version 3.2

LENGTH: 41
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APPLICANI: LV, NGGC
APPLICANI: Prentice, James
APPLICANT: Prentice, James
APPLICANT: MacDonald
APPLICANT: MacDonald
APPLICANT: MacBonald
APPLICANT: MacBonald
APPLICANT: Morris, MacDonald
APPLICANT: MORRIS, MacDonald
APPLICANT: Rosenberg, Steven
TITES OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT APPLICATION NUMBER: DC7/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-12-20
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PARCHILING VERSION 3.2
SEQ ID NO 2401
LENGTH: 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.3%; Score 37.5; DB 6; Length 441; 33.3%; Pred. No. 11; tive 5; Mismatches 6; Indels
                         APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2401, Application US/10511937 Publication No. US20060088836A1 GENERAL INFORMATION:
, Sequence 2947, Application US/10511937
, Publication No. US20060088836A1
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APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
                                                                                                                         Fry, Kirk
Woodward, Robert
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Best Local Similarity 33.38
Servative
Conservative
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US-10-511-937-2947
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                                                                               Score 35; DB 6; Length 651;
Pred. No. 48;
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W2-10-505-928-543
W2-10-505-928-543
Sequence 543, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
   APPLICANT: Ludwig Institute for Cancer Research et al.; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 2896/739178
; CURRENT FILING DATE: 2004-08-27
; CURRENT FILING DATE: 2004-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                       Gequence 142, Application US/09949925
publication No. US20060099575A9
GEMERAL INPORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 67 Human secreted proteins
FILE REFERENCE: PZ023P2
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 60/232,150
PRIOR PELING DATE: 1999-01-27
PRIOR PELING DATE: 1999-01-27
PRIOR PLING DATE: 1999-01-27
PRIOR PLING DATE: 1999-01-30
PRIOR FILING DATE: 1999-01-30
PRIOR PLILING DATE: 1999-01-30
PRIOR FILING DATE: 1999-01-30
PRIOR PLILING DATE: 1999-01-30
PRIOR PRILING DATE: 1999-01-30
PRIOR APPLICATION NUMBER: US 60/073,161
PRIOR PRILING DATE: 1999-01-30
PRIOR PLILING DATE: 1999-01-30
PRIOR PRILING DATE: 1999-01-30
PRIOR PLILING DATE: 1999-01-30
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Pred. No. 3.5;
3; Mismatches 3;
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COTHER INFORMATION: Xaa equals stop translation US-09-949-925-142
                                                                                                                                                     2; Mismatches
                                                                                  35.7%;
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Best Local Similarity 50.0%;
Matches 7; Conservative
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                                                                                                             Best Local Similarity 55.6
Matches 5; Conservative
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92 LRHFVGWVW 100
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ORGANISM: Homo sapiens
; ORGANISM: Homo
US-10-511-937-2401
                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-09-949-925-142
                                                                                         Query Match
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Sequence 109, Application US/11169140
Publication No. US20060099150A1
GENERAL INFORMATION:
APPLICANT: ARIZEEE PHARMACEUTICALS, INC.
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Best Local Similarity 42.1<sup>3</sup>
Matches 8; Conservative
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ORGANISM: Simian
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Sequence 5. Application US/11302678

Sequence 5. Application No. US2006008881A1

SEQUENCE 1. PROSMATION

MILLE SECTION STATE 
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Pred. No. 55;
3; Mismatches 4; Indels
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473 RRFTQSGDLYRHIRKFH 489
PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
SEQ ID NO 543
LENGTH: 522
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Best Local Similarity 47.1%;
Matches 8; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-505-928-543
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64 LGNVWRF 70
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RESULT 7 US-11-169-140-109

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APPLICANT: ARLEADE FURNICALED FUNCTION, LOW.

APPLICANT: HOUSTON, LOW.

APPLICANT: HARLEY, Stephen

APPLICANT: HARLEY, Stephen

APPLICANT: HARLEY, Stephen

APPLICANT: HARLEY, Stephen

APPLICANT: HARLEY, Steven

TITLE OF INVENTION: MATHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CEITILE OF INVENTION: MATHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CEITILE OF INVENTION: MARBER: US 10/11/69,140

CURRENT FILING DATE: 2005-06-27

PRIOR APPLICATION NUMBER: US 60/267,601

PRIOR PILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-10-02-0

PRIOR PRILING DATE: 2000-10-03-0

PRIOR PLING DATE: 2000-10-02

PRIOR PELING DATE: 2001-10-02

PRIOR PELING DATE: 2001-10-02

PRIOR PELING DATE: 2001-10-02

PRIOR PELING DATE: 2001-10-02

PRIOR FILING DATE: 2001-10-02

PRIOR FILING DATE: 2001-10-02

PRIOR FILING DATE: 2001-10-02

PRIOR FILING DATE: 2001-10-02

NUMBER OF SEQ ID NOS: 143

SOFTWARE: PATCHTIN VERSION 3.0

SEQ ID NO 109

TENTING DATE: 2001-10-02

NUMBER OF SEQ ID NOS: 143

SEQ ID NO 109
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Sequence 21, Application US/11024544A

PUBLICANT: US20060094086A1

SEGUENCE INFORMATION:
APPLICANT: E.I. dubont de Nemours and Company, Inc.
APPLICANT: Yadav, Narendra

APPLICANT: Yadav, Narendra

APPLICANT: Application
APPLICANT: Application
APPLICANT: Application
APPLICANT: Anany, Hongarian
APPLICANT: Chang, Hongarian
AUTILE OF INVENTION: FATTY ACIDS AND OIL CONTENT IN OLEAGINGUS ORGANISMS
FILE REFERENCE: CL2117
FILE REPERENCE: 2004-12-29

NUMBER OF SEQ ID NOS: 175

SOFTWARE: Patentin version 3.3

SEQ ID NO 21

LENGTH: 503
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DATABASE ENTRY DATE: 2003-10-31
RELEVANT RESIDUES: (1)..(503)
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Best Local Similarity 43.8%;
Matches 7; Conservative
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US-11-242-505A-48

US-11-242-505A-48

US-11-242-505A-48

Sequence 48. Application US/11242505A

Publication No. US20060099656A1

GENERAL INFORMATION:

APPLICANT: Carroll, Joseph M.

APPLICANT: Healy, Alileen

TITLE OF INVENTION: Methods and Compositions for Treating

TITLE OF INVENTION: Hearly, Alileen

TITLE OF INVENTION: Hearly, Alileen

TITLE OF INVENTION: Hearly, Aliles

TITLE OF INVENTION: Hearly, Aliles

TITLE OF INVENTION: Hearly, Aliles

TITLE OF INVENTION: Hamber: US 10/29, 078

FILE REFERENCE: MPI2001-288PIRCPIOMNIM

CURRENT APPLICATION NUMBER: US 10/290, 078

PRIOR APPLICATION NUMBER: US 10/390, 078

PRIOR PLING DATE: 2001-11-07

PRIOR PLING DATE: 2002-11-16

PRIOR PLING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: G0/341, 606

PRIOR APPLI
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Pred. No. 45;
1; Mismatches 2; Indels
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156 RRFV-STWKLIALVHG 170
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Best Local Similarity 50.0%;
Matches 5; Conservative
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SOFTWARE: PatentIn version 3.3
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Best Local Similarity 62.5
Local 5; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 342
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Sequence 87, Application US/11264784

Sequence 87, Application US/20060094092A1

GENERAL INFORMATION:

APPLICANT: E.I. duPont de Nemours & Co., Inc.

APPLICANT: Damude, Howard Glenn

APPLICANT: Maccol, Damid Joseph

APPLICANT: Maccol, Damid Joseph

APPLICANT: Maccol, Damid Joseph

APPLICANT: Ragghianti, James John

APPLICANT: Ragghianti, James John

APPLICANT: Ragghianti, James John

APPLICANT: Zhang, Hongxiang

APPLICANT: Zhang, Hongxiang

APPLICANT: Zhang, Woulnn

TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA

FILE REFERENCE: CL3136 USNA

CURRENT FILING DATE: 2005-11-01

NUMBER OF SEQ ID NOS: 375

SEQ ID NO 87

LENGTH: 503

LENGTH: 503

LENGTH: SO3
                                                                                                                                                                                                                        Sequence 135, Application US/11190750

Publication No. US20060094088A1

GENERAL INFORMATION:

APPLICANT: B.I. duPont de Nemours and Company, Inc.

APPLICANT: B.I. duPont de Nemours and Company, Inc.

APPLICANT: Yadav, Narendra

APPLICANT: Tanny, Hongxiang

TITLE OF INVENTION: ACYLTRANSPERASE REGULATION TO INCREASE THE PERCENT OF

TITLE OF INVENTION: POLYGNATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF

TITLE OF INVENTION: DLEAGINOUS ORGANISMS

FILE REFERENCE: CL2718

CURRENT PAPLICATION NUMBER: US/11/190,750

CURRENT FILING DATE: 2005-07-27

NUMBER OF SEQ ID NOS: 159

SOFTWARE: PatentIn version 3.3

LENGTH: 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Magnaporthe grisea 70-15 [GenBank Accession No. EAA52634] US-11-190-750-135
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34.2%; Score 33.5; DB 7; Length 503;
Best Local Similarity 43.8%; Pred. No. 64;
Matches 7; Conservative 3; Mismatches 5; Indels
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34.2%; Score 33.5; D
Best Local Similarity 43.8%; Pred. No. 64;
Matches 7; Conservative 3; Mismatches
                                          |||: | |: | :|
156 RRFV-STWKLIALVHG 170
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   3 RRFIGSIWRFIRAFYG 18
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; OTHER INFORMATION: DGAT1
US-11-264-784-87
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Pred. No. 50;
3; Mismatches 2; Indels
Sequence 7, Application US/11204427

Publication No. US20060100146A1

GENERAL INFORMATION:
APPLICANT: Stutiey, Stephen L
APPLICANT: Turkish, Aaron R

APPLICANT: Billheimer, Jeffrey T
APPLICANT: Billheimer, Jeffrey T
APPLICANT: ANTI-RELATED METHODS AND ARTICLES
TITLE OF INVENTION: AMAT-RELATED METHODS AND ARTICLES
FILE REPRENCE: 0575/17296/JPW/AJM/JCS

CURRENT APPLICATION NUMBER: US/11/204,427

CURRENT FILING DATE: 2005-08-15
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3 RRFIGSIWRFIRAFYG 18

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216 FCGOIWPVDQQFY 228
                           5 FIGSIWRFIRAFY 17
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                                                                                                                                        RESULT 15
US-11-242-505A-18
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Sequence 48, Application US/11304129

Publication No. US20060088915A1

GENERAL INFORMATION:

APPLICANT: OHTAKI, Tetsuya

APPLICANT: HAKATSU, Yoshihiro

APPLICANT: TERAO, Yasushi

APPLICANT: TERAO, Yasushi

APPLICANT: TERAO, Yasushi

APPLICANT: HINUMA, Yasushi

APPLICANT: HINUMA, Yasushi

APPLICANT: HINUMA, Syuji

TILE REFERENCE: 2762USOP

FILE REFERENCE: 2762USOP

CURRENT APPLICATION NUMBER: US/11/304,129

CURRENT FILING DATE: 2003-09-29

FRIOR PILING DATE: 2000-07-18

PRIOR FILING DATE: 2000-07-18

PRIOR FILING DATE: 2001-02-02

PRIOR FILING DATE: 2001-07-07

PRIOR FILING DATE: 2001-07-17

SEQ ID NO 48

LENGTH: 333

TWEND REQ ID NOS: 58

LENGTH: 333

TWEND REQ ID NOS: 58

LENGTH: 333
US-11-304-129-40

Sequence 40, Application US/11304129

Sequence 40, Application US/11304129

Publication No. US20060088915A1

GENERAL INFORMATION:

APPLICANT: CHTAKI, Tetsuya

APPLICANT: TAKATSU, Yoshihiro

APPLICANT: HINUMA, Syuji

TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof

FILE REFERENCE: 2762050

CURRENT APPLICATION NUMBER: US/11/304,129

CURRENT FILING DATE: 2003-09-29

PRIOR FILING DATE: 2000-07-18

PRIOR FILING DATE: 2000-07-18

PRIOR FILING DATE: 2000-07-18

PRIOR FILING DATE: 2001-02-02

PRIOR FILING DATE: 2001-02-02

PRIOR FILING DATE: 2001-07-17

WUMBER OF SEQ ID NOS: 58

SEQ 1D NO 40

LENGRIH: 393
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Pred. No. 58;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.7%; Score 33; DB 7; Length 393;
46.2%; Pred. No. 58;
tive 1; Mismatches 6; Indels
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Best Local Similarity 46.2
Matches 6; Conservative
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Matches 6; Conservative
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ORGANISM: Rat
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y GENERAL INFORMATION:
APPLICANT: Healy, Aileen
APPLICANT: Healy, Aileen
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 14717, 9941, 19310, c
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 14717, 9941, 19310, c
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 14717, 9941, 19310, c
TITLE OF INVENTION: Hematological Disorders Using 232, 2054, 1960, 14717, 9941, 19310, c
FILE REFERENCE: MPIZOL-28891RERS US/11/242,505A
CURRENT APPLICATION NUMBER: US/11/242,505A
CURRENT APPLICATION NUMBER: US 60/347,949
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 10/320,351
PRIOR PLING DATE: 2001-12-16
PRIOR APPLICATION NUMBER: 60/341,606
PRIOR APPLICATION NUMBER: 60/341,606
PRIOR APPLICATION NUMBER: 60/341,606
PRIOR APPLICATION NUMBER: 00/341,606
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR P
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; Sequence 18, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 44.4
Matches 4; Conservative
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155 VRRVLGAVW 163
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24 82 25 82 27 81					:	4 rv		RESULT 1	ID AD034338 st XX AD034338.	12-AUG-2	<pre>KW apolipoprot KW vasotropic; KW serum chole KW atheroscler</pre>	KW low-density XX OS Synthetic.	_	PD 27-MAY-2004 XX PF 13-NOV-2003		XX PA (UABR-) UAE	XX PI Anantharami	XX DR WPI; 2004-4	Synthetic	PI COMPTIBER S	PS Claim 4; SE XX	CC The inventi			CC the synthet	
						:					 											-				
5.1.8 Biocceleration Ltd.		Search time 94.2857 Seconds (without alignments) 87.287 Million cell updates/sec			នុម	ers: 2589679 .						cted by chance to have a of the result being printed, score distribution.		Description	Ado34338 Synthetic Ado34339 Synthetic	Ado34231 Synthetic Ado34354 Synthetic	Ado34225 Synthetic Ado34228 Synthetic	Ado34236 Synthetic Ado34340 Synthetic	Ado34233 Synthetic Ado34350 Synthetic	Ado34314 Synthetic Ado34352 Synthetic	Ado3429/ Synchetic Ado34244 Synthetic Ado34076 Synthetic	Ado34227 Synthetic	Ado34322 Synthetic	Ado34337 Synthetic	Ado34240 Synthetic Ado34344 Synthetic	
GenCore version 5. Copyright (c) 1993 - 2006 Bi	protein - protein search, using sw model	: May 19, 2006, 14:13:22 ; Se	US-10-712-447-116 t score: 98 ce: 1 GLRRFIGSIWRFIRAFYG 18	g table: BLOSUM62 Gapop 10.0 , Gapext 0.5	ed: 2589679 segs, 457216429 residues	number of hits satisfying chosen parameters:	m DB seq length: 0 m DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	4 : 1		 ••	Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score di	SUMMARIES *	Query Score March Length DB ID	98 100.0 18 8 98 100.0 18 8	94 95.9 18 8 94 95.9 18 8	94 95.9 18 8 94 95.9 18 8	94 95.9 18 8 94 95.9 18 8	94 95.9 18 8 94 95.9 18 8	91 92.9 18 8 90 91.8 18 8	88 89.8 18	86 87.8 18 8	85 86.7 18 8	84 85.7 18 8	83 84.7 18 8 83 84.7 18 8	
	OM pro	Run on	Title: Perfect Sequence	Scoring	Searched	Total	Minimum Maximum	Post-p	Database					Result No.	2 1	w 4	w w	i~ 00	201	12	111	- 11	1 27 7	i X F	222	

Ado34284 Synthetic		Ado34319 Synthetic	Ado34245 Synthetic							Ado34242 Synthetic		Ado34281 Synthetic	Ado34317 Synthetic	Ado34323 Synthetic		Ado34264 Synthetic		Ado34320 Synthetic	Aay18917 Lecithin:	Aay19171 Lecithin:
18 8 ADO34284	18 8 ADO34239	18 8 ADO34319	18 8 ADO34245	18 8 ADO34301	18 8 ADO34343	8	18 8 ADO34302	18 8 ADO34279	18 8 ADO34303	18 8 ADO34242	18 8 ADO34300	18 8 ADO34281	18 8 ADO34317	18 8 ADO34323	18 8 ADO34280	18 8 ADO34264	18 8 ADO34342	18 8 ADO34320	18 2 AAY18917	18 2 AAY19171
82 83.7	81 82.7	81 82.7	80 81.6		80 81.6		78 79.6	78 79.6					78 79.6	77 78.6	77 78.6	76 77.6	76 77.6	75 76.5	74 75.5	74 75.5
22.4	7 P	27	28	58	30	31	32	33	34	35	36	37	38	36	40	41	42	. 43	44	45

## ALIGNMENTS

apolipoprotein-E mimicking peptide, SEQ ID No 115. tandard; peptide; 18 AA 4 (first entry)

otein-E mimicking polypeptide, antilipaemic; cardiant;
c; antiarteriosclerotic; cerebroprotective; antianginal;
asterool, coronary artery disease; dysbetalipoproteinaemia;
arosis; myocardial infarction; stroke; embolus; angina;
cy lipoprotein; LDL; very low density lipoprotein; VLDL. 03-A2.

3; 2003WO-US036268. 4.

)2; 2002US-0425821P.

AB RES FOUND.

Datta G; ĎW, niah GM, Garber

411629/38.

apolipoprotein-E mimicking polypeptide useful for treating utery disease, dysbetalipoproteinemia or atherosclerosis an amino acid sequence. artery

SEQ ID NO 115; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypuocleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic

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apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (UDL) or a cell and enhances degradation of LDL or Ville by a cell. This sequence represents a synthetic apolipoprotein-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mimicking polypeptide of the invention.
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88686888888888888888

Sequence 18 AA;

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Gaps
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0
   100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 5.2e-08;
                               0; Indels
                                 0; Mismatches
                                                                               1 GLRRFIGSIWRFIRAFYG 18
                                                              1 GLRRFIGSIWRFIRAFYG 18
Query Match
Best Local Similarity 100.0
Marches 18, Conservative
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Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116.
ADO34339 standard; peptide; 18 AA.
          (first entry)
          12-AUG-2004
     ADO34339;
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apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL;

Synthetic

WO2004043403-A2 27-MAY-2004 13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

Datta G; Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 116; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polyynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

ö cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E minicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinemian or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E minicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL), to a cell and enhances degradation of LDL or very low to be a cell. This sequence represents a synthetic apolipoprotein-E Gaps mimicking polypeptide has the following activities: antilipaemic, .; 0 100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 5.2e-08; 0; Indels Mismatches mimicking polypeptide of the invention. ;; 0 GLRRFIGSIWRFIRAFYG 18 1 GLRRFIGSIWRFIRAFYG 18 Query Match
Best Local Similarity 100.
Matches 18; Conservative Sequence 18 AA;

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ADO34231 standard; peptide; 18 AA. RESULT 3 ADO3423

ADO34231;

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 8. 12-AUG-2004 (first entry) 

apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

Synthetic

WO2004043403-A2

27-MAY-2004.

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P.

UABR-) UAB RES FOUND

WPI; 2004-411629/38.

Anantharamiah GM,

ΰ

Garber DW,

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 8; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, myocardial infarction or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (UDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.

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Gaps

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Length 18;

95.9%; Score 94; DB 8; Le 88.9%; Pred. No. 2.1e-07; iive 2; Mismatches 0;

16; Conservative

Best Local Similarity

Query Match Matches

Sequence 18 AA;

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                                                                                                                                       low
cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for treating coronary artery disease, myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein. [DL] or very low density lipoprotein (VDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 131,
                                                                                                                                                                                                                                                      95.9%; Score 94; DB 8; Length 18; 88.9%; Pred. No. 2.1e-07; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Datta
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO34354 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                         1 GLRRFIGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                            Anantharamiah GM, Garber DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-NOV-2003; 2003WO-US036268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                       Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UABR-) UAB RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-411629/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004043403-A2
                                                                                                                                                                                                                             Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-AUG-2004
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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising
                                                                                                                                                                                                 Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
                                                                                                                                                                                                                           apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL;
                                                                                                                                                                                                                                                                                                                                                                                     'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; SEQ ID NO 2; 79pp; English
                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                           ADO34225 standard; peptide; 18 AA
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                1 GLRRFIGSIWRFIRAFYG
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                                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

Claim 4; SEQ ID NO 131; 79pp; English.

the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiareriosclerotic, cerebroprotective, and antiargainal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal cub as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for breaking and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (LDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention. 

Sequence 18 AA;

95.9%; Score 94; DB 8; Length 18; 88.9%; Pred. No. 2.1e-07; ive 2; Mismatches 0; Indels 18 1 GLRRFIGSIWRFIRAFYG Local Similarity 88.9 les 16; Conservative Query Match Best Loca Matches ò

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Gaps

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ADO34228 standard; peptide; 18 RESULT 6

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(first entry) 12-AUG-2004 ADO34228;

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 5.

vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL. apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; 

Synthetic.

WO2004043403-A2.

27-MAY-2004

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. Datta G; Anantharamiah GM, Garber DW, WPI; 2004-411629/38.

Claim 4; SEQ ID NO 5; 79pp; English

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide activities: antilipaemic, cardiant, vaeotropic, anticateriosclarotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, and slooperteinaemia or atherosclarosis, and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E ô The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic Gaps apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL, very low density lipoprotein; UDL. Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. monoclonal antibody that specifically binds to the synthetic ö Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 13. Score 94; DB 8; Length 18; Pred. No. 2.1e-07; 2; Mismatches 0; Indels 2; Mismatches ö mimicking polypeptide of the invention Claim 4; SEQ ID NO 13; 79pp; English. Datta Ä. ADO34236 standard; peptide; 18 1 GLRRFIGSIWRFIRAFYG 18 1 GIRRFLGSIWRFIRAFYG 18 Garber DW, 95.9%; 13-NOV-2003; 2003WO-US036268. 13-NOV-2002; 2002US-0425821P (first entry) Best Local Similarity 88.9 Matches 16; Conservative (UABR-) UAB RES FOUND. WPI; 2004-411629/38. Anantharamiah GM, Ą. WO2004043403-A2 12-AUG-2004 27-MAY-2004. Seguence 18 Synthetic. ADO34236; Query Match RESULT 7 ADO34236 

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apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiatteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan); for treating coronary artery disease, and also for treating angina. The synthetic apolipoprotein-E mimicking consisty lipoprotein-E mimicking of low-density lipoprotein-E mimicking chances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117
                                                                                                                                                                                                                                                                                                                                                        Score 94; DB 8; Length 18;
Pred. No. 2.1e-07;
2; Mismatches 0; Indels
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les 16; Conservative
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mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein. E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinedmenia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein. E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein. E mimicking mimicking polypeptide of the invention.
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Pred. No. 2.1e-07;
2; Mismatches 0; Indels
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antianginal. The synthetic apolipoprotein-E minicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysberalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E minicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (LDL) to a cell and enhances degradation of LDL or mimicking polypeptide of the invention.
cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
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95.9%; Score 94; DB 8; Length 18; 88.9%; Pred. No. 2.1e-07; ive 2; Mismatches 0; Indels
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                                                         1 GLRRFIGSIWRFIRAFYG
               Local Similarity 88.5
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Matches
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18 1 GIRRFLGSIWRFIRAFYG

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 127. ADO34350 standard; peptide; 18 AA. (first entry) 12-AUG-2004 ADO34350; RESULT 10 

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease, dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

Synthetic

WO2004043403-A2.

27-MAY-2004

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND.

Datta G; Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 127; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic and apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and actrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide and activities and mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

Claim 4; SEQ ID NO 91; 79pp; English.

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antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or oranguten); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke, for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or WLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
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88.9%;
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                                                                                                                                                                                                    Sequence 18 AA;
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ADO34314
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useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atheroclerosis; and for reducing the risk of myccardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (ULDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
                         88888888888888
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Gaps
                                 ö
 Length 18;
92.9%; Score 91; DB 8; 1
83.3%; Pred. No. 6.2e-07;
ive 3; Mismatches 0;
                                                               GLRRFIGSIWRFIRAFYG 18
   Query Match 92.9
Best Local Similarity 83.3
Matches 15; Conservative
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Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 129.
     ADO34352 standard; peptide; 18 AA
                12-AUG-2004 (first entry)
           ADO34352;
RESULT 12
  AD034352
```

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant, vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL;

Synthetic.

WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

ö Datta Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. Claim 4; SEQ ID NO 129; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide acomposition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E cardiant, vasotropic, antiarteriosolerotic, cerebroprotective, and antiandinal. The synthetic apolipoprotein-E mimicking serum cholesterol in a subject (including a mammal

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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and arribody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide as the following activities: antilipaemic, and antianteriosclerotic, cerebroprotective, and carrieriaclectoric, cerebroprotective, and carrieriaclectoric as untianginal. The synthetic apolipoprotein-E mimicking polypeptide is untianginal. The synthetic apolipoprotein-E mimicking polypeptide is untianginal as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
                                                                                                                                                                                                                                                                                              ö
           chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breading an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vāsotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
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rat, rabbit, cow, shedp, pig, human, monkey, ape,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 74.
                                                                                                                                                                                                                                                 Score 90; DB 8; Length 18;
Pred. No. 8.9e-07;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO34297 standard; peptide; 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-2003; 2003WO-US036268.
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                                                                                                                                                                                                                                                        91.8%;
                                                                                                                                                                                                                                                                                                                                                                1 GLRRFIGSIWRFIRAFYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                14; Conservative
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                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anantharamiah GM,
    a mouse,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004043403-A2.
                                                                                                                                                                                                                Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADO34297;
  such as
                                                                                                                                                                                                                                                                                                  Matches
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chimpanzee or orangutan); for treating coronary artery disease, dysbetaliopproteinsenia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking oblypeptide enhances binding of low-density lipoprotein (IDL) or very low density lipoprotein (VIDL) to a cell and enhances degradation of IDL or VIDL by a cell. This sequence represents a synthetic apolipoprotein-E
                                                                                                                                                                                                              mimicking polypeptide of the invention
      88888888888
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Gaps
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89.8%; Score 88; DB 8; Length 18; 77.8%; Pred. No. 1.8e-06; ive 4; Mismatches 0; Indels
                                                              1 GLRRFIGSIWRFIRAFYG 18
             Local Similarity 77.8 les 14, Conservative
 Query Match
                  Best Loc
Matches
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18 

ADO34244 standard; peptide; 18 (first entry) 12-AUG-2004 ADO34244; RESULT 14 ADO34244 

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 21.

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apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholestroni, coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL;

Synthetic

WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

Anantharamiah GM, Garber DW,

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WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 21; 79pp; English

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymenticle is a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic and activities antilippement. C apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease,

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypudleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide and a carrier; and apolipoprotein-E mimicking polypeptide activities: antilipaemic, cardiant, vasotropic, antiatreriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

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dysbetalipoproteinaemia or atherosclerobis; and for reducing the risk of myocardial infarction or stroke, for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein. Emimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein. Emimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .18
/note= "All Lys residues are DiMethyl-Lysine"
                                                                                                                                                                                                                                                                                                                                                                                           Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 53.
                                                                                                                                             Score 88; DB 8; Length 18;
Pred. No. 1.8e-06;
                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Datta G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; SEQ ID NO 53; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                       ADO34276 standard; peptide; 18 AA.
                                                                                                                                                                                                                     1 GLRRFIGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garber DW,
                                                                                                                                             89.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-2002; 2002US-0425821P.
                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anantharamiah GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004043403-A2
                                                                                                                   Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                     AD034276;
                                                                                                                                               Query Match
                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                           RESULT 15
ADO34276
    88888888888
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useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein. E mimicking polypeptide enhances binding of low-density lipoprotein (ULD) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein. E mimicking polypeptide of the invention.
                888888888888888
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ö Gaps ö Query Match

89.8%; Score 88; DB 8; Length 18;
Best Local Similarity 77.8%; Pred. No. 1.8e-06;
Matches 14; Conservative 4; Mismatches 0; Indels

ò g

Search completed: May 19, 2006, 14:24:31 Job time: 95.2857 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

May 19, 2006, 14:24:57; Search time 14.2857 Seconds (without alignments) 121.233 Million cell updates/sec

US-10-712-447-116 98 1 GLRRFIGSIWRFIRAFYG 18

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\*

1: pirl: \* 2: pir2: \* 3: pir3: \* 4: pir4: \* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		d				
Result		Query	1	c c	£.	מסייות ייייסססר
No.	score	March	marcn Lengtn	9 :	J.D.	Describrion
-	48		627	7	S76462	hypothetical prote
7	47	48.0	516	7	T33269	hypothetical prote
ო	45	45.9	489	~	B84733	probable cytochrom
4	44	•	246	~	I54412	HLA-A CE
ហ	44		273	-	нгние9	н
φ	44	44.9	365	ч	HLHUA2	н
7	44	44.9	365	~	I38443	HLA-A-0
ω	44	4	365	~	161902	class I
σ	44	44.9	365	~	137542	class I
10	44	44.9	365	7	I84448	class I hi
11	44	44.9	365	~	161857	MHC HLA-A2.4a chai
12	44	44.9	365	~	I38442	gene HLA-A-0205 pr
13	44	4	589	8	A34341	poly (3-hydroxybuty
14	43	43.9	503	~	B81690	probable sodium-tr
15	43	43.9	519	Н	T02263	cytochrome P450 DW
16	42.5	43.4	760	~	E84953	penicillin-binding
17	42	42.9	139	~	G64032	_
18	42	42.9	214	~	D72540	hypothetical prote
19	42	42.9	237	~	B72692	_
20	42	42.9	537	~	T04745	
21	42	42.9	785	~	S63652	
22	42	42.9	806	7	A84060	leucyl-tRNA synthe
23	42	42.9	861	7	H64102	leucine-tRNA ligas
24	42	42.9	1112		T42383	probable calcium-a
25	41.5	42.3	1025		AH3568	acriflavin resista
26	41	41.8	178		A75578	transcription regu
27	41	41.8	265	7	T32316	ŭ
28	41	41.8	265		425	
29	41	41.8	359	~	T20575	hypothetical prote

hypothetical protein C24B9.13 - Caenorhabditis elegans
hypothetical protein C24B9.13 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004
C; Accession: T33269
B; Murray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D.
B; Murray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D.
B; Murray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D.
B; Marca cumber: Z21310
A; Reference number: Z21310
A; Accession: T33269
A; Status: preliminary; translated from GB/SWBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-516 < MURA
A; Residues: 1-516 < MURA
A; Residues: 1-516 < MURA
A; Cross-references: UNIPROT: O76442; UNIPARC: UPIO00007D477; EMBL: AF068709; PIDN: AAC19257.13
A; Experimental source: strain Bristol N2; clone C24B9

48.0%; Score 47; DB 2; Length 516; 52.9%; Pred. No. 9.8;

Query Match Best Local Similarity

C;Genetics: A;Gene: CESP:C24B9.13 A;Map position: 5 A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2

hypothetical prote probable permease DNA ligase (NAD) (	hypothetical prote TMV resistance pro receptor tyrosine	probable transcrip phosphosterase re phosphosterase re	nypothetical proce o-antigen export s o-antigen export s	NADH2 dehydrogenas conserved hypothet	Conserved Aypornet F3H9.12 protein - purine permease [i
AF2599 G97381 AG3325	S57161 T04583 T30938	T52113 G75297	T32318 F71707 D97700	T13684 E90444	A87395 C86408 D86408
000	000	000	200	00	000
364 364 719	1584 1607 2051	107	251 258 258	303	338 351 356
41.8 41.8 41.8	41.8 41.8 11.8	40.8 40.8	40.8 40.8 8.0.8	40.8 40.8	4 4 4 4 4 4 4 4 4 4 6 9 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
444	444	44	4 4 4 0 0 0	4 4 0 0	4 4 4 0 0 0
30 31 32	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	36	8 8 8 8 6 0	41	4 4 4 5 4 3

## ALIGNMENTS

		RESULT 1 S76462 hypothetical protein - Synechocystis sp. (strain PCC 6803) C;Species: Synechocystis sp.
		A;Varlety: FCL 9903 Date: 25:PCT #8equence_revision 25-Apr-1997 #text_change 09-Jul-2004 C:Accession: 376462
		R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
		DNA Res. 3, 109-136, 1996 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
. •	.,	8. A.Reference number: S74322; MUID:97061201; PMID:8905231 A.Accession: S76462
-	. •	A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA
		A; restruces: 1-2.7 x xxxxx x x x x x x x x x x x x x x x
		Query Match 49.0%; Score 48; DB 2; Length 627; Best Local Similarity 38.9%; Pred. No. 8.2; Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
		Qy 1 GLRRFIGSIWRPIRAFYG 18    : :      ::      :   b 597 GLEQLLGKIWQWLRQKFG 614

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Mismatches

3,

Conservative

.. 6

Matches

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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-365 < KOL>
A;Cross-references: UNIPARC:UPI0000124E24; GB:K02883; NID:g187605; PIDN:AA98727.1; PID:g
A;Experimental source: 1,Wiphobbastoid cell line 721
A;Experimental source: 1,Wiphobbastoid cell line 721
B;Ennis, P.D.; Zemmour, J.; Salter, R.D.; Partim, P.
Proc. Natl. Acad. Sci. U.S.A. 87, 2833-2837, 1990
A;Title: Rapid cloning of HLA-A, B cDNA by using the polymerase chain reaction: frequency A;Reference number: A35997; MUID:90207291; PMID:2320591
A;Molecule type: mRNA
A;Cross-references: UNIPARC:UPI0000124E24; GB:M84379; GB:M32322; NID:g403143; PIDN:AAA596
A;Note: this allele is designated A*0201 (previously HLA-A2.1)
B;Krangel, M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHC class I histocompatibility antigen HLA-A2 alpha chain precursor [validated] - human c, Species: Homo sapiens (man) (pate: 28-Reb-1980 #sequence revision 22-Apr-1995 #text_change 08-Dec-2000 C; Accession: I55948; E35997; A02191; S19020; S77965; S23593; A93834; A93919; S14802; A021 R; Roller, B.H.; Orr, H.T.
J. Immunol. 134, 2727-2733, 1985
A,Title: Cloning and complete sequence of an HLA-A2 gene: Analysis of two HLA-A alleles & A,Reference number: I55948; MUID:8513272; PMID:2982951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPARC:UPI00001737ED; EMBL:X57954; NID:g32150
A;Note: this allele is designated A*0204
A;Note: the sequence in GenBank entry HSHLAA020, release 106.0, (PID:g32151) differs beck R;Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBO J. 4, 1205-1210, 1985
A;Title: Unusual RNA splicing generates a secreted form of HLA-A2 in a mutagenized B lymp
A;Reference number: A02191, MUID:85230571; PMID:3874058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 South American Indians. Spatial cl
                                                                                                                                                                                                                                                                                                                                                                             A,Map position: 6p21.3-6p21.3
A;Introns: 89/3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen F;195-260/Domain: immunoglobulin homology <IMM>
F;85/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Residues: 39-365 < KRA>
A; Residues: 39-365 < KRA>
A; Residues: 39-365 < KRA>
A; Cross-references: UNIPARC:UPI000016AA56; GB:X02457; NID:g32153; PIDN:CAA26297.1;
A; Note: the author translated the codon CAG for residue 96 as His, ACU for residue 8 Thr, and ACU for residue 323 as Ser
B; Castano, A.R.; Lopez de Castro, J.A.
Immunogenetics 34, 281-285, 1991
A; Title: Structure of the HLA-A*0204 antigen, found in South American Indians. Spat
A; Reference number: S19020; MUID:92039809; PMID:1937577
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                                   class I molecules.
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Pred. No. 16;
                                                                                                   A;Accession: B24671
A;Molecule type: DNA
A;Residues: 1-273 <HOL>
A;Cross-references: UNIPROT:P10316; UNIPARC:UP10000124E4B
EMBO J. 4, 2849-2854, 1985
A;Title: Exon shuffling in vivo can generate novel HLA 6
A;Reference number: A91021; MUID:86055720; PMID:3877632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                     A, Gene: GDB:HLA-A
A, Cross-references: GDB:119310; OMIM:142800
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A; Residues: 9-120,'M', 122-365 < CAS1>
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50.0%;
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102 VGSDWRFLRGYH 113
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Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
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Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: I54412
R;Arnot, D.; Lillie, J.W.; Auffray, C.; Kappes, D.; Strominger, J.L.
Immunogenetics 20, 237-252, 1984
A;Title: Inter-locus and intra-allelic polymorphisms of HLA class I antigen gene mRNA.
A;Reference number: I54412; MUID:84287690; PMID:6332068
A;Accession: I54412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: UNIPROT: Q9ZV72; UNIPARC: UPI000009D8ED; GB: AE002093; NID: G3831452;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P450 homology
                                                                                                                                                                                                                                                                                                                                     probable cytochrome P450 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B94733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MHC HLA-A cell surface antigen - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
   Gaps
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C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome
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Pred. No. 14;
4; Mismatches 2; Indels
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       Indels
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A Status: preliminary A Molecule type: DNA A;Residues: 1-489 <STO> A; Accession: B84733

A;Gene: At2g32440

Genetics:

IGNMWSFLRAF 64 IGSIWRFIRAF

RESULT 4

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA A;Residues: 1-246 <RES>

C; Superfamily: crace \_\_\_\_\_\_C; Keywords: surface antigen C; Keywords: surface antigen F;101-166/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative

IGSIWRFIRAFY 17 8 VĞSDWRFLRGYH 19

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RESULT 5

A;Residues: 1-365 <BEL> A; Molecule type: mRNA

Accession: A93834

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A,Cross-references: GDB:119310; OMIM:142800
A,Cross-references: GDB:13-6p21.3
C,Superfamily: class I histocompatibility antigen; immunoglobulin homology
C,Superfamily: class I bistocompatibility antigen; immunoglobulin homology
C,Reywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>F;1-24/Domain: signal sequence #status predicted +sp25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predicF;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predicF;220-285/Domain: immunoglobulin homology <IMM>
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MHC class I histocompatibility antigen HLA-A alpha chain precursor - human (isolate A*02)
CiSpecies: Homo sapiens (man)
A;Variety: isolate A*0212
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 23-Jul-1999
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A;Experimental source: cell line KRC 033; isolate A*0212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPARC:UP1000016A06E; EMBL:U03863; NID:9432438; PIDN:AAA03604.1; PII C;Superfamily: class I histocompatibility antigen; immunoglobulin homology F;220-285/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                   R;Holmes, N.; Ennis, P.; Wan, A.M.; Denney, D.W.; Parham, P. J. Immunol. 139, 936-941, 1987
A;Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A28
A;Reference number: 138441; MUID:87252273; PMID:3496393
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R; Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.;
Rstelich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.;
Rstelich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.;
Rstelich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.;
Rstelich Musch and M. Williams, M.
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C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C;Accession: 137542; S49582
R;Barouch, D.; Krausa, P.; Bodmer, J.; Browning, M.J.; McMichael, A.J.
Immunogenetics 41, 388, 19;
A;Title: Identification of a novel HIA-A2 subtype, HIA-A*0216.
A;Reference number: 137542; MUID:95278976; PMID:7759139
                                                               C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: 138443
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Pred. No. 21;
4; Mismatches 2; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-365 <RES>
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Pred. No. 21;
4; Mismatches
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Conservative
               gene HLA-A-0203 protein - human
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 25-55, 2',57-60, 'B',62, 'B',64-66, 'Z',68-74, 'X',76-85, 'RXXX',90-94,'AH',97,'V
A; Residues: 25-55, 2',57-60, 'B',62, 'B',64-66,'Z',68-74,'X',76-85,'RXXX',90-94,'AH',97,'V
A; Cross-references: UNISAC:UPIO001037380
A; Arcoss-references uniques: US-8 and His Strong, D.M.; Orr, H.T.
A; Lopez de Castro, J.A.; Strominger, J.L.; Strong, D.M.; Orr, H.T.
Arcos: Natl. Acad. Sci. US-8, 79, 3813-3817, 1982
A; Article: Structure of crossreactive human histocompatibility antigens HLA-A2 A; Reference number: A93919; MUID:82247941; PMID:6179086
                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPARC:UP10000124E24; EMBL:M84379; NID:g403143; PIDN:AAA59606.1; PI A;Experimental source: cell line GRC 138; isolate A*0201
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
R;Castano, A.R.; Lopez de Castro. J.A.
Immunogenetics 35, 344-346, 1992
A;Title: Structure of the HLA-A *0211 (A2.5) subtype: further evidence for selection-dri
A;Reference number: S23593; MUID:92218010; PMID:1559719
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A; Residues: 25-85, TXXXX, 90-94, AH', 97, VV, 99-112, Z', 114-118, 'LZ', 121-125, 'X', 127-131,'
A; Residues: 25-85, TXXXX, 90-94, AH', 97, VV, 99-112, Z', 114-118, 'LZ', 121-125, 'X', 127-131,'
A; Residues: 25-85, EX, 267-294 aLOP
A; Cross-references: UNIPARC: UP100001737EF
R; Silver, M.L.; Parker, K.C.; Wiley, D.C.
A; Title: Reconstitution by MHC-restricted peptides of HLA-A2 heavy chain with beta-2-mic
A; Reference number: S14802; MUID:91204056; PMID:2017257
A; Accession: S14802
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A;Map position: 6p21.3-6p21.3
A;Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1; 365/1
A;Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1; 365/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Superfamily: class I histocompatibility antigen; transmembrane protein; transplantati
F;1-34/Domain: signal sequence #status predicted <SIG>
F;25-365/Product: MHC class I histocompatibility antigen HLA-A2 alpha chain #status expe
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A;Molecule type: mRNB
A;Roledues: 9-96,'ID',99-365 <CAS2>
A;Residues: 9-96,'ID',99-365 <CAS2>
A;Residues: 9-96,'ID',99-365 <CAS2>
A;Cross-references: UNIPARC:UPI000008AF57; EMBL:X60764; NID:g32156; PIDN:CAB56609.1; IA;Note: this allele is designated A*0211 (previously HLA-A2.5)
R;Orr, H.T.; Lopez de Castro, J.A.; Parham, P.; Ploegh, H.L.; Strominger, J.L.
R;Orr, H.T.; Lopez de Castro, J.A.; Parham, P.; Ploegh, H.L.; Strominger, J.L.
A;Orr, H.T.; Lopez de Castro, J.A.; Parham, P.; Ploegh, H.L.; Strominger, J.L.
A;Title: Comparison of amino acid sequences of two human histocompatibility antigens, A;Reference number: A93834; MUID:80056745; PMID:92029
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F;220-285/Domain: immunoglobulin homology <IMM>
F;220-285/Domain: transmembrane #status predicted <TWM>
F;310-331/Domain: intracellular #status predicted <IMT>
F;110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;125-188,227-283/Disulfide bonds: #status predicted
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Nature 357, 326-329, 1992
A.Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.
A.Reference number: 137120; MUID:92269955; PMID:1317015
A.Accession: S77965
                                                                                                                                                                                                                             Status: nucleic acid sequence not shown; translation not shown
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Pred. No. 21;
4; Mismatches 2; Indels
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A;Molecule type: protein A;Residues: 25-36 <SIL> A;Cross-references: UNIPARC:UP100001737F0

A;Gene: GDB:HLA-A

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127 VGSDWRFLRGYH 138
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RESULT I38443

44.98; 50.0%;

Query Match Best Local Similarity

Conservative 6 IGSIWRFIRAFY 17

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Matches

RESULT 10

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A;Residues: 1-219 <SCH>
A;Cross-references: UNIPARC:UPIO00016E162; GB:M64341; NID:g141964; PIDN:AAA21979.1; PID:g
A;Note: the authors translated the codon TAC for residue 120 as Thr
C;Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Resdues: 1-599 < PED.
A;Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:g141958; PIDN:J
A;Experimental source: strain H16
B;Schubert, P; Krueger, N.; Steinbuechel, A.
A; Schubert, P; Krueger, N.; Steinbuechel, A.
A; Status in 173, 168-175, 1991
A;Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cispecies: Alcaligenes eutrophus
Cipates 12-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
Cipates 12-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
Cipates 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
Ripeoples, O.P.; Sinskey, A.J.
Biol. Chem. 264, 15298-15303, 1989
A;Title: Poly-beta-hydroxyburyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Ident A;Reference number: A34341; MUID:89359357; PMID:2670936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   generation of the HLA-A2/A28
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I38442
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44.9%; Score 44; DB 2; Length 589;
Best Local Similarity 47.6%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 5; Indels
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                                        Indels
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A.Title: Multiple genetic mechanisms have contributed to the A.Feference number: 138441; MUID:87252273; PMID:3496393
A.Accession: 138441; MUID:87252273; PMID:3496393
A.Accession: 138441; Multiple from GB/EMBL/DDBJ
A.Molecule type: DNA
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Pred. No. 21;
4; Mismatches
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127 VGSDWRFLRGYH 138
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127 VGSDWRFLRGYH 138
                                            Conservative
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A; Status: preliminary
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I38442
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C;Species: Homo sapiens (man)
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;Superfamily: class I histocompatibility antigen; immunoglobulin homology
;220-285/Domain: immunoglobulin homology <IMM>
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                                                                             A;Cross-references: UNIPARC:UP1000016AA63; EMBL:Z46633; NID:g575248; PIDN:CAA86602.1; A;Note: submitted to the EMBL Data Library, November 1994
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Nature 357, 326-329, 1992
Affitle: Unusual HLA-B alleles in two tribes of Brazilian Indians.
A;Reference number: 137120; MUID:92269955; PMID:1317015
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C;Species: Homo sapiens (man)
C;Date: 02-01-1996 #sequence_revision 02-011-1996 #text_change 09-Jul-2004
C;Date: 02-01-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 161857
B;Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A;Title: Diversity and diversification of HLA-A,B,C alleles.
A;Reference number: 136956; MUID:99235215; PMID:2715640
A;Status: preliminary, translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1365 *RES>
A;Const. 1265 *RES>
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C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
                                                                                                                                                      C,Genetics:
A,Gene: hla-A
C,Superfamily: class I histocompatibility antigen; immunoglobulin homology
P,220-285/Domain: immunoglobulin homology <IMM>
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Pred. No. 21;
4; Mismatches
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Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 4; Mismatches
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A;Status: translated from GB/EMBL/DDBJ
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Best Local Similarity 50.0%;
Matches 6; Conservative
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127 VGSDWRFLRGYH 138
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        A; Molecule type: mRNA
A; Residues: 1-365 < RES>
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Query Match

RESULT 14

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probable sodium-translocating NADH dehydrogenase (ubiquinone) (EC 1.6.5.-) ngrB chain TC c;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Dacession: B81690 F;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, A;Reference number: 881590 MJD:20150255; PMID:10684935 A;Reference number: A81500; MUD:20150255; PMID:10684935 A;Ression: B81690                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9PKB6; UNIPARC:UPI0000057982; GB:AE002323; GB:AE002160; NIQ
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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43.9%; Score 43; DB 1; Length 519;
Best Local Similarity 54.5%; Pred. No. 43;
Matches 6; Conservative 3; Mismatches 2; Indels
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Pred. No. 42;
4; Mismatches 3; Indels
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Best Local Similarity 46.2
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: TC0550
C,Keywords: oxidoreductase
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T02263
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Search completed: May 19, 2006, 14:39:58 Job time : 15.2857 secs

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Sequence:

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Database

Result Š

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Q56yel arabidopsie
Q4bfm2 burkholderi
Q2jito cyanobaccer
Q3m6c5 anabaena va
Q8x308 rallecnia s
Q9c5y2 arabidopsis
Q9c5y2 arabidopsis
Q9c1b7 fuarxium sp
Q9c1b7 fuarxium sp
Q5gh65 mus musculu
Q5gh67 rattus norv
Q5gh57 rattus norv
Q5gh73 homo sapien
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLECTIDE SEQUENCE.

de Kort C.A.D., Koopmanschap A.B.;
"Nucleotide and deduced amino acid sequence of a cDNA clone encoding diapause protein 1, an amylphorin-type storage hexamer of the Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;
Q8kba7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       670 AA; 79825 MW; 8A000BA115BEC8A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X76080; CAA53691.1; -; mRNA.
HSSP; P04253; ILL1.
G0; G0:0005344; F:oxygen transporter activity; IEA.
G0; G0:006810; P:transport; IEA.
InterPro; IPR00896; Hemcoyanin.
InterPro; IPR005203; hemcoyanin.
InterPro; IPR005203; hemcoyanin.
PANTHER; PTHR11511; Hemcoyanin.
Pfam; PF03723; Hemcoyanin.
Pfam; PF03722; Hemcoyanin.
Pfam; PF03722; Hemcoyanin.
Pfam; PF03722; Hemcoyanin.
N: 1.
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Pred. No. 9.8;
6; Mismatches
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PROSITE; PS00210; HEMOCYANIN_2; UNKNOWN_1.
                 ©56YS1_ARATH
04BRAZ_BURVI
02JITO_9CYAN
03M6C5_ANAVT
08XG08_RALSO
RXAOZ_ARATH
084ZW0_PEA
000857_FUSSP
09C187_FUSSP
05CH65_MOUSE
05CH65_MOUSE
XXRR6_ATH
XRR6_ATH
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J. Insect Physiol. 40:527-535(1994)
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Q25271;
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les 7, Conservative
 376
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513
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   Leptinotarsa.
NCBI_TaxID=7539;
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Q3APYS CHLCH
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144.247 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                     2849598
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Q3APY5 CHLCH
Q84ZW1 PEA
Q9F7V7 RHILV
Q2NUB5 SODGL
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O76442_CAEEL
Q39L57_BURS3
Q456F4_9BURK
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Q7W7P3_BORPA
Q7WL31_BORBR
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XKR7 PANTR
XKR7 MOUSE
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O32N49 XENLA
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Listing first 45 summaries
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Q3PK79 ]
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2: uniprot_trembl:*
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98
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Maximum DB seq length: 200000000
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NCBI_TaxID=387;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Vagnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                           US DOE Joint Genome Institute;
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Bryant D., Schmutz J., Larimer F., Land M., Kyrpides N., Ivanova N., Richardson P.;
"Complete sequence of Chlorobium chlorochromatii CaD3.";
Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22417727; PubMed=12529541; DOI=10.1104/pp.012963; Davidson S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.; The pea gene NA enrodes ent-kaurenoic acid oxidase."; Plant Physiol. 131:335-34(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                    Leucyl-tRNA syntherase class Ia (EC 6.1.1.4).
OrderedLocusNames=Cag_1688;
OrderedLocusNames=Cag_1688;
OrderedLocusNames=Cag_1688;
OrderedLocusNames=Cag_1688;
Chlorobium chlorobia; Chlorobiales; Chlorobiaceae;
Chlorobium/Pelodictyon group; Chlorobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.1%; Score 54; DB 2; Length 805; 53.8%; Pred. No. 12; 2; Indels iive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; CP000108; ABB28940.1; -; Genomic_DNA.
GO; GO:000524; F.ATP binding; IEA.
GO; GO:000423; F.leucine-tRNA ligase activity; IEA.
GO; GO:0016874; F.ligase activity; IEA.
GO; GO:0016429; P.leucyl-tRNA aminoacylation; IEA.
Aminoacyl-tRNA synthetase; Complete profecome; Ligase.
SEQUENCE 805 AA; 92007 MW; AOC78883732AF54C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
-!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF537321, AAC23063.1; -; mRNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0020037; F:heme binding; IEA.
GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0004872; F:metal ion binding; IEA.
GO; GO:0004497; F:monooxygenase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003, integrated into UniProtKB/TrEMBL 01-JUN-2003, sequence version 1.
                   22-NOV-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      488 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003, sequence version 1.
07-FEB-2006, entry version 21.
Ent-kaurenoic acid oxidase.
                                           22-NOV-2005, sequence version 1.
21-FEB-2006, entry version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: ||:| :||:
622 GISRFLGKVWRFV 634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 53.8
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
TISSUE=Shoot;
                                                                                                                                                                                                          NCBI_TaxID=340177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
Q84ZM1 PEA
LD Q84ZM1 PEA
AC Q84ZM1 PEA
DT 01-JUN-2003,
DT 01-JUN-2003,
DT 07-FEB-2006,
DE Entr-Kautenoi
GN Name=KAOJ;
OS Pisum Sativu
OC Entraryota; V
OC Spermatophytic
OC TOSIGS; euro
OX NOBI TaxID=3
RN (1)
RP NUCLEOTIDE &
RC TISSUE=Shoot
RX The pea ger
RY The pea ger
CC --- SIMILAR;
CC ---- S
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Matches
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                           ö
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR001201; ER4501.
PANTHER; PTR1819383; Cytochrome_P450; 1.
Pfam; PF00067; P450; 2.
PRINTS; PR000463; EP4501.
PRNTS; PR00086; CYTOCHROME_P450; UNKNOWN_1.
BROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
BROSITE; PS00086; CYTOCHROME_P450; WRNOWN_1.
BROGADSamic reticulum; Heme; Iron; Membrane; Metal-binding; Monocoxygenase; Oxidoreductase.
SEQUENCE 488 AA; 56478 MW; 503453CB6E43C830 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobium leguminosarum bv. viciae.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001, integrated into UniProtKB/TrEMBL. 01-MAR-2001, sequence version 1. 07-FEB-2006, entry version 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                735 AA.
                                                                                                                                                                                                                                    Score 51; DB
Pred. No. 21;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF273216; AAG25076.1; -; Genomic_DNA.
HSSP; P08716; 1MT0.
                                                                                                                                                                                                                                                                                                                                                                                                          V7 RHILV
QSF7V7_RHILV PRELIMINARY; PRT;
Q9F7V7;
                                                                                                                                                                                                                                      52.0%;
                                                                                                                                                                                                                                                        Local Similarity 66.7 es 8; Conservative
                                                                                                                                                                                                                                                                                                               5 FIGSIWRFIRAF 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABC transporter RzcB.
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Gaps

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4; Indels

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                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/Terms
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Larimar F., Land M.;
Annotation of the draft genome assembly of Paracoccus denitrificans pD1222.";
                                                                                                                       EMBL, BA000045; BAC89304.1; -; Genomic_DNA.
BioCyc, GV10251221:GLL1363-MONOMER; -.
GO; GO:0004040; F:amidase activity; IEA.
GO; GO:00004545; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.
InterPro; IPR002503; Amidase_3 hydro.
InterPro; IPR002901; Amidase_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Paracoccus.
NCBI_TaxID=318586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Gli
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Paracoccus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 2; Length 401;
Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                       401 AA; 44051 MW; 903814BB688C170B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AAIT01000001; EAN68115.1; -; Genomic_DNA.
GO; GO:0020037; F:heme binding; IEA.
GO; GO:0005505; F:iron ion binding; IEA.
GO; GO:0046972; F:metal ion binding; IEA.
GO; GO:0004497; F:menooxygenase activity; IEA.
GO; GO:0004118; P:electron transport; IEA.
InterPro; IPR001128; Cytcochrome_P450.
InterPro; IPR0012401; EP4501.
Pfam; PF00067; p450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-0CT-2005, integrated into UniProtKB/TrEMBL. 25-0CT-2005, sequence version 1. 07-FEB-2006, entry version 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          449 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                   Pfam; PF01520; Amidase 3; 1. Pfam; PF01832; Glucosaminidase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 49.0%;
Local Similarity 69.2%;
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Q3PK79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 GLERFIRGYWRFI 116
DNA Res. 10:137-145(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GLRRFIGSIWRFI 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
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STRAIN=PD1222;
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MEDLINE=22977040; PubMed=14621292; DOI=10.1093/dnares/10.4.137;
Makamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
Kohara M., Matsumoto M., Marsuno A., Nakazaki N., Shimpo S.,
Takeuchi C., Yamada M., Tabata S.;
Tcomplete genome structure of Gloeobacter violaceus PCC 7421, a
cyanobacterium that lacks thylakoids.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Bacteria; Cyanobacteria; Gloeobacteria; Gloeobacterales; Gloeobacter.
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Massive genome erosion and functional adaptations provide insights into the symbiotic lifestyle of Sodalis glossinidius in the taetse host.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sodalis glossinidius str. 'morsitans'.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Sodalis.
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                                                                                    2; Length 735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toh H., Weiss B.L., Perkin S.A.H., Yamashita A., Oshima K.
Hattori M., Aksoy S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                              4; Indels
                             80717 MW; 0216259241F3630C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 AA; 40247 MW; 1257F70F3C3CA6EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-FEB-2006, integrated into UniProtXB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                   361 AA
                                                                              Match 51.0%; Score 50; DB Local Similarity 56.2%; Pred. No. 47; es 9; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP008232; BAE74260.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY; PRT;
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     PROSITE; PS50990; PEPTIDASE_C39; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-2003, sequence version 1. 07-FEB-2006, entry version 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , sequence version 1.
                                                                                                                                                                                                                                        | | |: :|||: |||
161 GFRWFLPAIWRYRRAF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putative glycosyltransferase
ORFNames=SG0985;
                                                                                                                                                                                                   1 GLRRFIGSIWRFIRAF 16
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62 RDVGSFWRFLSAF 74
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Best Local Similarity 61.5
Matches 8; Conservative
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                                     735 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=343509;
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                                                                                                                                                                                                                                                                                                                                                                        BS_SODGL
QZNUBS_SODGL
Q2NUBS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7NKW3 GLOVI
Q7NKW3;
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07-MAR-2006
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                                  SEQUENCE
                                                                                             Query Match
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Matches
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Detter C., Glavina T.,

XX-related protein 7./FTId=PRO\_0000190788.

Potential Potential

Potential

Potential Potential Potential

4

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EMBL; AY534245; AAT07094.1; -; mRNA.
EMBL; AL031658; CAB88102.1; ALT_SEQ; Genomic_DNA.
Ensembl; SNSG000010131; Homo sapiens.
MROC; HGNC:23062; XKR7.
Membrane; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XKR7 PANTR
Q49LS1;
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                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XKR7 PANTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a; MEDLINE M., Babbage A.K., Bagguley C.L., MEDLINE M., Babbage A.K., Bagguley C.L., MEDLINE M., Basaley O.E., Blakey S.E., Bridgeman A.M., Brown A.J., Basaley O.E., Burtel M.D., Carder C., Carter N.P., Clamp M., Clark D., Dunn M., Coulson A., Coville G.J., Deadman R.E., Dhami P.D., Dunn M., Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., Blington A.G., Frankland J.A., Fraser A., French L., Garner P., Ammond S., Harley J.L., Heath P.D., How S., Holden P.J., Hurkle E., Hunt A.R., Hunt S.E., Jekosech K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehvaeslahlo M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McLay K., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Thompe A., Swann R.M., Sycamore N., Taylor R., Thompe N., Thorpe A., Swann R.M., Sycamore N., Taylor R., Thomas D.M., Thorpe A., Swann R.M., Sycamore N., Taylor R., Thomas D.M., Thorpe A., Whitehead S.L., Whitteker P., Willey D.L., Williams L., Williams S.A., Willing D.L., Whitehead S.L., Whitteker P., Willey D.L., Williams L., Wi
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential).
-!- SIMIJARITY: Belongs to the XK family.
-!- CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 414:865-871(2001).
-!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huang C.-H., Chen Y.; "A superfamily of XX-related genes (XRG) widely expressed in vertebrates and invertebrates."; Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                     DB 2; Length 449;
PRINTS; PR00463; EP4501.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
Heme; Iron; Metal-binding; Monooxygenase; Öxidoreductase.
SEQUENCE 449 AA; 50659 MW; 5F3EEC9E12AA3B35 CRC64;
                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                               O5GH72; O9NUGS;
11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
01-MAR-2005, sequence version 1.
07-FEB-2006, entry version 8.
                                                                                                                                                                                                                                                                                                 579 AA.
                                                                                                                    Pred. No. 59;
1; Mismatches
                                                                                                    Query Match
Best Local Similarity 80.0%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                     Name=XKR7; Synonyms=C20orf159, XRG7;
                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                        8; Conservative
                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                         7 GSIWRFIRAF 16
                                                                                                                                                                                                ||:||||| |
13 GSVWRFIRDF 22
                                                                                                                                                                                                                                                                                                                                                                                    KK-related protein 7.
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                 HUMAN
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XXR7 HUMAN
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                                                                                                                                                                                                                                                                                              13-SEP-2005, sequence version 1.
07-FEB-2006, entry version 6.
NAK-related protein 7.
Name=XKR7; Synonyms=XRG7;
Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Ptimates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huang C.-H., Chen Y.:
"A superfamily of XK-related genes (XRG) widely expressed in
"A superfamily of XK-related genes (XRG) widely expressed in
"A superfactes and invertebrates.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-: SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
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Pred. No. 77;
                                                Score 48; DB 1; Length 579;
Pred. No. 77;
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6DFE1191093E85D4 CRC64;
Potential.
D8D0FF64B9EDD53D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XK-related protein 7.
/FTId=PRO 0000190790.
Potential.
                                                                                                                                                                                                                                                                              11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                             579 AA.
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                                                                                    4; Mismatches
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Potential.
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                                                                                                                                                                                                                                             PRT;
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                  63826 MW;
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63593 MW;
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                                                  49.0%;
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190 LGQVWRYLRALY 201
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Matches 6; Conservative
                                                                                                                      6 IGSIWRFIRAFY 17
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                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Membrane; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79
109
280
334
375
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89 1
260 2
314 3
355 3
384 4
415 4
415 4
579 AA;
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Matches 6; Conserv
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                             Huang C.-H., Chen Y.; "A superfamily of XK-related genes (XRG) widely expressed in "A superfamily of XK-related "A superfamily of XK-solates"; "Submitted (19AN-2004) to the EMBL/GenBank/DDBJ databases."; Submitted (19AN-2004) to the EMBL/GenBank/DDBJ membrane protein -: SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48; DB 1; Length 580;
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F3291FABF4C5A826 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          XX-related protein 7.
/FIId-PRO_000190789.
Potential.
Potential.
Potential.
Potential.
Potential.
Potential.
Potential.
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                                      11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      580 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                         EMBL; AY534253; AAT07102.1; -; mRNA.
Ensembl; ENSWUSG0000042631; Mus musculus.
MGI; MGI:3526711; Xkr7.
Membrane; Transmembrane.
                                                                                                                                                                                                                                                                                (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potentia]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
             PRT;
                                                 01-MAR-2005, sequence version 1.
07-FEB-2006, entry version 10.
NAr-celated protein 7.
Name=Kkr7; Synonyme=Krg7;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64302 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.0%;
50.0%;
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STRAIN=Sprague-Dawley;
Huang C.-H., Chen Y.;
                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [MRNA].
STRAIN=C57BL/6J;
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190 LGQVWRYLRALY 201
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               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 580 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxiD=10116;
                                                                                                                                                          NCBI_TaxID=10090;
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9
XXR7_MOUSE
ID _XXR7_MOUSE
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ID XKR7_RAT
AC Q5GH56;
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                          Q5GH64;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Galagan J.E., Calvo S.E., Cuomo C., Ma L.-J., Wortman J.R.,
Batzoglou S., Lee S.-I., Bastuerkmen M., Spevak C.C., Clutterbuck J.,
Kapitonov V., Jurka J., Scazzocchio C., Farman M., Buller J.,
Burcell S., Harris S., Braus G.H., Draht O., Busch S., D'Enfert C.,
Bouchier C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S.,
Doonan J.H., Yu J., Vienken K., Pain A., Freitag M., Selker E.U.,
Archer D.B., Penalva M.A., Oakley B.R., Momany M., Tanaka T.,
Kumagai T., Asai K., Machida M., Nierman W.C., Denning D.W.,
Caddick M., Hynes M., Paoletti M., Fischer R., Miller B.L., Dyer P.S.,
Sachs M.S., Osmani S.A., Birren B.W.;
"Sequencing of Aspergillus nidulans and comparative analysis with A.
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fumigatus and A. oryzae.";
Nature 438:1105(2005).
-: CAUTION: The sequence shown here is derived from an
-:- EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                              -i- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
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superfamily of XK-related genes (XRd) widely expressed in
                                                                                                                                                                                                                                                                                                                                                                                 Score 48; DB 1; Length 580;
Pred. No. 77;
4; Mismatches 2; Indels
                  vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0015205; F:nucleobase transporter activity; IEA.
                                                                                                                                                                                                                                                                                                                                                       8F4907F391B4F5BE CRC64;
                                                                                                                                                                                                       /FTId=PRO_0000190791.
                                                                                                                                                                                        protein 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QSAUSS_EMENI PRELIMINARY; PRT; 597 AA. QSAUSS.
QSAUSP.
26-ARR-2005, integrated into UniProtKB/TrEMBL.
26-APR-2005, sequence version 1.
07-MAR-2006, entry version 6.
OT-MAR-2006, entry version 6.
ORFVNAMES=AN7955.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=FGSC 4;
PubMed=16372000; DOI=10.1038/nature04341;
                                                                  (Potential).
-!- SIMILARITY: Belongs to the XK family
                                                                                                                                                                                          XX-related
                                                                                                                                                                                                                                                                        Potential. Potential.
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Eurotiales, Trichocomaceae, Emericella.
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                                                                                                                                                                                                                                                                                                                                                        64338 MW;
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                                                                                                                                                                                                                                                                                                                                                                                      49.0%;
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190 LGQVWRYLRALY 201
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                                                                                                                                                                                Membrane; Transmembrane
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                                                                                                                                                                                                                                                                                                                                                        580 AA;
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3303
3326
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TRANSMEM
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RESULT 15
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GO; GO:0015931; P:nucleobase, nucleoside, nucleotide and nucl. . .; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Okumura S.,
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                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDLINE=970601201; PubMed=8905231; DOI=10.1093/dnares/3.3.109;
MEDLINE=970601201; PubMed=8905231; DOI=10.1093/dnares/3.3.109;
Kaneko T., Sato S., Kocani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
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13-SEP-2005, sequence version 1.
21-FEB-2006, entry version 9.
Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
CHORNAMES=ClimDRAFT_1980;
CHORODALM Infincola DSM 245.
CHORODALM CHOLODAL, Chlorobia; Chlorobiaceae;
Chlorobium/Pelodictyon group; Chlorobium.
                                                                            Query Match 49.0%; Score 48; DB 2; Length 597; Best Local Similarity 47.1%; Pred. No. 79; Matches 8; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
        InterPro; IPR001248; Cyt. pur. permease.
Pfam; PF02133; Transp_cyt_pur; 1.
Hypothetical protein.
SEQUENCE 597 AA; 65089 MW; E686F4978F37BF5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               627 AA; 69725 MW; BBE187A53BF96229 CRC64;
                                                                                                                                                                                                                                                                                                  Sll1858 protein.
OrderedLocusNames=sll1858;
Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
                                                                                                                                                                                                                                                          01-FEB-1997, integrated into UniProtKB/TrEMBL. 01-FEB-1997, sequence version 1. 07-FEB-2006, entry version 29.
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                                                                                                                                                                                                                                  627 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BA000022; BAA18591.1; -; Genomic_DNA.
PIR; S76462; S76462.
BioCyc; SSP1148:SLL1858-MONOMER; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h Similarity 38.9%; Score 48; Similarity 38.9%; Pred. No. 67; Conservative 6; Mismatch
                                                                                                                                                                                                                                P74489 SYNY3 PRELIMINARY; PRT; P74489;
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                                                                                                                                                     159 LRSFVGCMWFGMQAFWG 175
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044QD1 CHLLI
DQ QQD101
CHLLI
DQ QQD01,
DT 13-SEP-2005, integrated into Ur
DT 13-SEP-2005, sequence version 1
DT 21-FEB-2006, entry version 9.
DE Leucyl-tRNA synthetase bacteris
GN ORFNames=ClimDRAFT 1980;
GS Chlorobium limicola DSM 245.
OC Bacteria; Chlorobi; Chlorobia;
OC Chlorobium/Pelodictyon group; OX NCBI TaxID=290315;
RN [1]
                                                                                                                                     2 LRRFIGSIWRFIRAFYG 18
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Best Local Similarity
Matches 7; Conserval
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Distributed under the Creative Commons Attribution-NoDerivs License
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US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Incas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
Sequencing of the draft genome and assembly of Chlorobium limicola DSM 245.";
                                                                                                                                                                                                                                                                                                US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Chlorobium limicola DSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Chlorobium phaeobacteroides DSM 266.";
                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Chlorobium/Pelodictyon group; Chlorobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48; DB 2; Length 805; Pred. No. 1.1e+02; 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-SEP-2005, integrated into UniProtKB/TrEMBL.
13-SEP-2005, sequence version 1.
21-FEB-2006, entry version 9.
Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
ORFNAMES=Cpha266DRAFT_2546;
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US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Chlorobium phaeobacteroides DSM 266.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.-
-: CAUTION: The sequence shown here is derived from an
                                                                                                                                                                   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AAHJO1000009; EAM43320.1, -; Genomic_DNA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004829; F:Leucine-tRNA ligase activity; IEA.
GO; GO:0006429; F:Leucine-tRNA minoacylation; IEA.
InterPro; IPR002302; Leu tRNASyn_la.
Pfam; PF00133; LRNA-synt_l; 1.
PRINTS; PR00985; TRNASYNTHLEU.
TIGRFAM; TIGR00396; leus_bact; 1.
Aminoacyl-tRNA synthetase.
SEQUENCE 805 AA; 91997 MW; D4F3FE28F9E92DF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      816 AA.
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Chlorobium phaeobacteroides DSM 266
Pacteria: Chlorope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Best Local Similarity 46.2%;
Matches 6; Conservative
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Q43K01;
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622 GISRFLGKVWRLV 634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary data.
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STRAIN=DSM 266;
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                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
STRAIN=DSM 245;
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EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

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Best Local Similarity 46.2%; Pred. No. 1.1e+02;
Matches 6; Conservative 4; Mismatches 3; Indels
                                                                                                              EMBL; AAIB01000002; EAM35935.1; -; Genomic_DNA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0006429; F:leucine-tRNA ligase activity; IEA.
GO; GO:0006429; F:leucine-tRNA ligase activity; IEA.
InterPro; IPR002302; Leu tRNAsyn_la.
Pfam; PF00133; tRNA-synt_l; 1.
PRINTS; PR00395; TRNASYNTHLEU.
TIGRFAMS; TIGR00395; leuS_bact; 1.
Aminoacyl-tRNA synthetase.
SEQUENCE 816 AA; 93335 MW; 6770B1DAC50560F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       1 GLRRFIGSIWRFI 13
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622 GISRFLGKVWRLV 634
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Search completed: May 19, 2006, 14:38:14 Job time : 116.429 secs

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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Buttner, Klaus
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Ocrnut, Isabelle
APPLICANT: Mource, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTY: USA
ZID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASESQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REPRENCE/POCKET NUMBER: 00915
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: No. 6004925e
US-08-940-095-242
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
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Sequence 343, App
Sequence 34, App
Sequence 34, App
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63.384 Million cell updates/sec
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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
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5: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-465-719-242
US-09-453-838-242
US-09-453-841-242
US-09-453-841-242
US-09-453-841-242
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US-09-453-836-242
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US-08-488-379-3
US-08-480-190-3
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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98
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Match Length
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Perfect score:
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## ALIGNMENTS

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STRANDEDNESS: sin
TOPOLOGY: linear
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US-09-465-719-242
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Sequence 242, Application US/08940093

Patent No. 6037324

GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Gekul, Rabelle
APPLICANT: Gornut, Isabelle
APPLICANT: Gornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Nevention: 258

CORRESPONDENCE: 258

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREE: NY

STREE: NY

STREE: NY
                                                                           Gaps
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Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1. Tandele
   Length 18;
                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTEY: NA
COMPUTEY: NA
ZIP: 10036-2811
COMPUTER: EDAMALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,093
FILING DATE: 29-5EP-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 30,0919
FILING DATE: APPLICATION NUMBER: 30,742
REFERENCE/POCKET NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REFERENCE/POCKET NUMBER: 30,742
REPRENCE/POCKET NUMBER: 30,743
REPRENCE/POCKET NUMBER: 30,743
REPRENCE/POCKET NUMBER: 30,743
REPRENCE/POCKET NUM
Score 74; DB 2; I
Pred. No. 3.9e-05;
6; Mismatches 1;
                                                                                                                                                                                       1 GLRRFIGSIWRFIRAFYG 18
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TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6037323e
   Query Match
Best Local Similarity 61.1%;
Matches 11; Conservative
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RESULT 3
US-08-940-096-242
; Sequence 242, Papplication US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:

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APPLICANT: Descui, vecus.
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Mccr. Gunther
APPLICANT: Mccr. Gunther
APPLICANT: Mccr. Gunther
APPLICANT: Mccr. Gunther
APPLICANT: Mccr. AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBERS OF SEQUENCES: 288:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STREET: 10036-2811
COMPUTER: BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FactSEQ Version 2.0
CUNTRY: USA
TILING DATE: 9-SEP-1997
CLASSIFTCATION NUMBER: US/08/940,096
FILING DATE: 9-SEP-1997
CLASSIFTCATION NUMBER: 30,742
APPLICATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
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Sequence 242 Application US/09465719
Relear No. 6265377
GENERAL INFORMATION:
APPLICANT:
Dasseux, Jean-Louis
APPLICANT: Sexul, Renate
APPLICANT: Sexul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunher
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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1155 Avenue of the Americas
Dasseux, Jean-Louis
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
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Best Local Similarity
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Dufourcq, Jean
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APLICANT: Dufourcq, Jean
APPLICANT: Severe APPLICANT: Jean
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                     009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 75.5%; Score 74; DB 2; I Best Local Similarity 61.1%; Pred. No. 3.9e-05; Matches 11; Conservative 6; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
APPLICATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6329341e
SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-453-605-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZUP: 110.36-2811
ZUP: 10.036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PRATEGQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
              REPERENCE/DOCKET NUMBER: 00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-453-838-242
; Sequence 242. Application US/09453838
Patent No. 6376464
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                              LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GIKKFLGSIWKFIKAFVG 18
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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Cornut, Isabelle
Metz, Guncher
Metz, Guncher
Difourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 258
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              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM:
SOCTWARE: FastSEQ Version 2.0
SOCTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
FILING DATE: CLASSIFICATION NUMBER: 08/940,093
FILING DATE: 29-SED-1997
ATTORNEY/AGENT INFORMATION:
NAME: COTUZI, LAUTA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
RELEPANS: 650-493-556
TELEPHONE: 650-493-556
TELEPHONE: 650-493-556
TELEPHONE: 650-493-556
TELEPANS: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 mmino acids
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COMPUTER: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASESCO VERSION 2.0
CURRENT APPLICATION NUMBER: US/09/453,605
FILLING DATE: 26-NO. 612931-1999
CLASSIFICATION: AUNKNOWN:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Mismatches
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FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 242, Application US/09453605
Patent No. 6329341
GENERAL INFORMATION:
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Best Local Similarity 61.11
Matches 11; Conservative
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COMPUTER READABLE FORM:
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STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-09-453-605-242
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Sequence 242, Application US/09453841
                                 GENERAL INFORMATION:
APPLICANT: Dassew
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US-09-453-833-242
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                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Mctz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: GENE THERAPY APPROACHES TO
TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
TITLE OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
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                                   Score 74; DB 2; Length 18;
Pred. No. 3.9e-05;
6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 75.5%; Score 74; DB 2; Length 18; Best Local Similarity 61.1%; Pred. No. 3.9e-05; Matches 11; Conservative 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30,742
.mp. 009196-0007-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REMANDAL

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,136
FILING DATE: 29-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: B.4PLICATION DATA:
APPLICATION NUMBER: FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: COTUZZI, LBUTA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-000
TELECHONICATION INFORMATION:
TELECHONE: 650-493-4935
TELEFAX: 6614 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
TENGTH: 18 mmino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                            Sequence 242, Application US/08940136
Patent No. 6518412
GENERAL INFORMATION:
                                                                                                                                    1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GIKKFLGSIWKFIKAFVG 18
                                                                                                               1 GLRRFIGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GLRRFIGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: No. 6518412e
                                       75.5%;
                                 Query Match
Best Local Similarity 61.1:
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRIE 2811
ZIP: 10036-2811
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                  JS-08-940-136-242
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 US-09-453-838-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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RESULT 8 US-09-453-841-242

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Sequence 242, Application US/09453833
Sequence 242, Application US/09453833
Septent No. 660284
GENERAL INFORMATION:
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Gornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT:
                                 APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30,742
FR: 009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: Fact SEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,841
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 08/940,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pennie & Edmonds LLP
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 0091
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GIKKFLGSIWKFIKAFVG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: No. 6573239e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDUJUM TYPE: DISKETTE
COMPUTER: IEM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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ATTORIES OB 940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LBUTR A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-556
TELEFAX: 650-493-556
INFORMATION FOR SEQ. ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRSTESQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,840
FILLIG DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: Pennie & Edmonds LLP
: 1155 Avenue of the Americas
New York
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Patent No. 6716816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GLRRFIGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: No. 6630450e

US-09-453-826-242
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                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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US-09-453-840-242
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Sequence 242, Application US/09453826

Settle No. 6630450

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Sekul, Renate

APPLICANT: Schul, Renate

APPLICANT: Gunther

APPLICANT: Dufourcq, Jean

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds Lip

STREET: 1155 Avenue of the Americas

CITY. New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                     COMPUTRY: USA
ZIP: 10036-2811
COMPUTRY: READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: TEASTEM: DOS
SOFTWARE: TEASTEM: DOS
SOFTWARE: TEASTEM: DOS
SOFTWARE: TEASTEM: DOS
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATE:
TALING DATE:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: COCULZI, LAURA
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-5556
INFORMATION FOR SEO ID NO: 242:
SEQUENCE CHARACTERISTICS:
TENERAL 18 BMINO acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10036-2811
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRAISEQ Version 2.0
CURRENT ARPLICATION DATA:
APPLICATION NUMBER: US/09/453,826
STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GLRRFIGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: No. 6602854e
US-09-453-833-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-09-453-826-242
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bastel, Render APPLICANT: Sekul, Render APPLICANT: Sekul, Render APPLICANT: Buttner, Klaus APPLICANT: Buttner, Klaus APPLICANT: Cornut, Isabelle APPLICANT: Metz, Gunther Gunt Jean APPLICANT: Difourcq, Jean TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS: 258
CORRESPONDENCE ADDRESS: Semine & Edmonds LLP STREET: 1155 Avenue of the Americas
Query Match
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-10-283-599-242
               RESULT 13
US-09-453-834-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-453-834-242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                  Query Match 75.5%; Score 74; DB 2; Length 18; Best Local Similarity 61.1%; Pred. No. 3.9e-05; Matches 11; Conservative 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 75.5%; Score 74; DB 2; Length 18; Best Local Similarity 61.1%; Pred. No. 3.9e-05; Matches 11; Conservative 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: No. 6734169e; SEQUENCE DESCRIPTION; SEQ ID NO: 242: US-09-865-989-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION UNIBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-865-989-242
i Sequence 242, Application US/09865989
i Patent No. 6734169
i GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ. ID NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GLRRFIGSIWRFIRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
        ; STRANDESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 258
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                RESULT 12
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GENERAL INFORMATION:

APPLICANT: Basseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Metz, Gunther
APPLICANT: Metz, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 242, Application US/10283599
| Patent No. 6644327 |
| GENERAL INFORMATION: |
| GENERAL INFORMATION: |
| APPLICANT: Dasseux, Jean-Louis |
| APPLICANT: Sekul, Renate |
| APPLICANT: Sekul, Renate |
| APPLICANT: Cornut, Isabelle |
| APPLICANT: Ornut, Isabelle |
| APPLICANT: Diffourcq, Jean |
| APPLICANT: Diffourcq, Jean |
| TITLE OF INVENTION: GENE THERAPY APPROACHES TO |
| TITLE OF INVENTION: GENE THERAPY APOLIPOPROTEIN A-1 AGONISTS AND THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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61.1%; Pred. No. 3.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REPERENCE/DOCKET NUMBER: 009196-0004-999
TELEPHONE: 650-491-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORPUTER: 1155 Avenue of the Americas STREET: 1155 Avenue of the Americas CITY: New York STATE: NY COUNTRY: USA ZIP: 10036-281 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM COMPATIER: IBM COMPATIER: IBM COMPATIER: OPERATING SYSTEM: DOS SOFTWARE: FRAESEQ Version 2.0 CURRENT APPLICATION DATA: FILING DATE: CLASSIFICATION:
Sequence 242, Application US/09453834 Patent No. 6753313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GLRRFIGSIWRFIRAFYG 18
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: No. 6753313e
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Search completed: May 19, 2006, 14:42:55 Job time : 24.8571 secs
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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Pred. No. 3.9e-05;
                                                                                                                                                                                                                     MEDIUM TIPE: DISKETCE
COMPUTER: DISKETCE
CORPUTER: DISKETCE
CORPUTER: DOS
SOCTWARE: FRATERO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,599
FILING DATE: 29-0CT-2002
CLASSIFICATION WUMBER: 08/940,136
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: 60-193-1936
FILEPHONE: 650-493-556
TELEPHONE: 650-493-556
TELEPHONE: 650-493-556
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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Patent No. 6900177
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: No. 6844327e US-10-283-599-242
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Best Local Similarity 61.1%;
Matches 11; Conservative
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                 ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                    USA
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STATE: N
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                    FILING DATE: 17-Dec-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
APPLICATION NUMBER: US/08/940,096
APPLICATION NUMBER: STILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COLUZI, LUMER: 30,742
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0005-999
TELECHONE: 650-493-4935
TELEFAX: 650-493-556
TELEFAX: 650-493-556
TELEFAX: 650-493-556
TELEFAX: 650-493-556
TELEFAX: 611 PENNIE
INFORMATION FOR SEQ. ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 maino acide
APPLICATION NUMBER: US/09/465,718
FILING DATE: 17-Dec-1999
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19, Appl 56, Appl 79, Appl 79, Appl 80, Appl 94, Appl 100, Appl 110, Appl

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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

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                                                                  Sequence
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US-10-712-447-22
US-10-712-447-78
US-10-712-447-195
US-10-712-447-19
US-10-712-447-19
US-10-712-447-58
US-10-712-447-58
US-10-712-447-77
US-10-712-447-79
US-10-712-447-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Matches 18; Conservative
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US-10-712-447-116
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      LENGTH: 18
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117, App

127, App

121, App

129, Appl

129, Appl

129, Appl

14, Appl

112, Appl

113, Appl

113, Appl

114, Appl

117, Appl

121, 
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| FMC Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
| FMC Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep: *
| FMC Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep: *
| FMC Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep: *
| FMC Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep: *
| FMC Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep: *
| FMC Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep: *
                                                                                                                                                   May 19, 2006, 15:18:19 ; Search time 81.2857 Seconds (without alignments) 102.575 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 1
Sequence 1
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                          GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-712-447-116
US-10-712-447-2
US-10-712-447-3
US-10-712-447-10
US-10-712-447-10
US-10-712-447-117
US-10-712-447-117
US-10-712-447-117
US-10-712-447-117
US-10-712-447-129
US-10-712-447-129
US-10-712-447-129
US-10-712-447-118
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US-10-712-447-82
US-10-712-447-16
US-10-712-447-96
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                                                                                                                                                                                                                                                                                                                                                                                           2097797 segs, 463214858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                - protein search, using sw model
                                                                                                                                                                                                                                                                                   1 GLRRFIGSIWRFIRAFYG 18
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Gapop 10.0 , Gapext 0.5
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98
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Maximum DB seq length: 200000000
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Query
Match Length DB
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Score

Result No.

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Gaps

Gaps

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Length 18;

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Sequence 10, Application US/10712447
; Sequence 10, Application NUS/10712447
; Publication NO. US20040186057A1
; GENERAL INFORMATION.
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: GARBER, DAVID W.
; TITLE OF INVENTION: SYMTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: SOOLIEPPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR APPLICATION NUMBER: 60/425,821
; ROFIGHARE: PATENT OS: 210
; SEQ ID NO 10
; SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: GARBER, DAVID W.
APPLICANT: GARBER, DAVID W.
APPLICANT: DATTA,
GETTA
APPLICANT: DATTA,
GETTA
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILE REFERENCE: 112739-123US
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT FILING DATE: 2003-11-13
PRIOR FILING DATE: 2002-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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88.9%; Pred. No. 4.7e-07;
                                                                                                                                                                                                                                                     95.9%; Score 94; DB 4; 88.9%; Pred. No. 4.7e-07;
                                                                                                                                                                                                                                                                                                     2; Mismatches
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Publication No. US20040186057A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 8
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GLRRFIGSIWRFIRAFYG 18
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                                                                                                       ORGANISM: Artificial Sequence
            SOFTWARE: Patentin Ver. 3.2
                                                                                                                                                                                                                                                                           Best Local Similarity 88.9
Matches 16; Conservative
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Matches 16; Conservative
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US-10-712-447-8
                              SEQ ID NO 5
LENGTH: 18
TYPE: PRT
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US-10-712-447-5
Sequence 5, Application US/10712447
Publication No. US20040186057A1
GENERAL INFORMATION:
APPLICANT: APPLICANT: DATH, GETA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPPEROTEIN E AND METHODS OF USE
TITLE OF INVENTION: US/10/712,447
CURRENT FILING DATE: 2003-11-13
PRIOR PELLING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: ARABER, DAVID W.
APPLICANT: DATTA, GEETA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILE REFERENCE: 112739-123US
CURRENT APPLICATION NUMBER: US/10/712,447
FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: 60/425,821
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PALENTIN VET: 3.2
SEQ ID NO 2
ENOTH: 18
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: peptide US-10-712-447-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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Publication No. US20040186057A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 116
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Sequence 117, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: ANNTHARAMIAH, GATTADAHALLI M.

APPLICANT: GARBER, DAVID W.

APPLICANT: GARBER, DAVID W.

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

FILE REFERENCE: 12739-1230S

CURRENT PILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

PRIOR FILING DATE: 2002-11-13

SOFTWARE: Patentin Ver. 3.2

SEQ ID NO 117

LENGTH: 18
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                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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                                                                                                                                                                                                                                                                   Query Match 95.9%; Score 94; DB 4; Length 18; Best Local Similarity 88.9%; Pred. No. 4.7e-07; Matches 16; Conservative 2; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
FEATURE:
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 88.9
Matches 16; Conservative
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Sequence 131, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ANNATHARAMIAH, GATTADAHALLI M.
APPLICANT: ANATHARAMIAH, GATTADAHALLI M.
APPLICANT: DATTA, GEETA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILE REFERENCE: 112739-123U8
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT APPLICATION NUMBER: 60/425,821
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
SEQ ID NOS: 210
SOFTWARE: PatentIN Ver. 3.2
SEQ ID NO 131
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ANANTHERANIAH, GATTADAHALLI M.
APPLICANT: ANANTHERANIAH, GATTADAHALLI M.
APPLICANT: GARBER, DAVID W.
APPLICANT: GARBER, DAVID W.
APPLICANT: DATTA, GEBTA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILE REFERENCE: 112739-123US
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT FILING DATE: 2002-11-13
PRIOR PILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
SPRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 210
SSEQ ID NOS: 210
SSEQ ID NO 127
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US-10-712-447-127
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic;; OTHER INFORMATION: peptide
US-10-712-447-117
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                                                                                                                    Query Match 95.9%; Score 94; DB 4; Length 18; Best Local Similarity 88.9%; Pred. No. 4.7e-07; Matches 16; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 127, Application US/10712447; Publication No. US20040186057A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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US-10-712-447-131
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US-10-712-447-127
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1 GIRRFLGSLWRFLRAFYG 18
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ORGANISM: Artificial Sequence
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Best Local Similarity 77.8%;
Matches 14; Conservative
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LOCATION: (3)
OTHER INFORMATION: (DIMe)Lys
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SOFTWARE: PatentIn Ver. 3.2
  14; Conservative
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LENGTH: 18
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Sequence 91, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: BANTHARAMIAH, GATTADAHALLI M.

APPLICANT: BATTA, GESTA

TITLE OF INVENTION: APOLIPPOROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPPOROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPPOROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPPOROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPPOROTEIN E AND METHODS OF USE

TITLE OF INVENTION UNMBER: US/10/712,447

CURRENT APPLICATION NUMBER: 60/425,821

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENTIN Ver. 3.2

SEQ ID NO 91

LENGTH: 18
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Publication No. US20040186057A1

GENERAL INFORMATION:
APPLICANT: GARBER, DAVID W.
APPLICANT: GARBER, DAVID W.
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
TITLE OF INVENTION APOLIPOPROTEIN E AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT APPLICATION NUMBER: 00/425,821

PRIOR FILING DATE: 2003-11-13

NUMBER OF SEQ ID NOS: 210

SEQ ID NO 129

LENGTH: 18
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US-10-712-447-91
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                         Length 18;
                                                                   0; Indels
                    Score 94; DB 4; I
Pred. No. 4.7e-07;
2; Mismatches 0;
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                       Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity
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US-10-712-447-53

$ Sequence 53, Application US/10712447

$ Publication No. US20040186057A1

$ Publication No. US20040186057A1

$ GENERAL INFORMATION:

$ APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

$ APPLICANT: GARBER, DAVID W.

$ APPLICANT: DATTA, GEETA

$ TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

$ TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

$ TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

$ TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

$ TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

$ TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

$ FILE REFERENCE: 112739-123US

$ CURRENT APPLICATION NUMBER: US/10/712,447

$ PRIOR FILING DATE: 2002-11-13

$ NUMBER OF SEQ ID NOS: 210

$ SOFTWARE: PATCHIN Ver. 3.2

$ SEQ ID NO 53

** LENGTH: 18

** MUMBER OF SEQ ID NO 53

** MUMBER OF SEQ ID NO 54

** MUMBER OF SEQ ID NO 54

** MUMBER OF SEQ ID NO 54

** MUMBER OF SEQ ID NO 55

** MUMBER OF SEQ ID NO 54

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| Sequence 21, Application US/10712447
| Sequence 21, Application No. US20040186057A1
| Publication No. US20040186057A1
| GENERAL INFORMATION:
| APPLICANT: AMANTHARAMIAH, GATTADAHALLI M.
| APPLICANT: GARBER, DAVID W.
| APPLICANT: GARBER, DAVID W.
| APPLICANT: GARBER, DAVID W.
| TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING |
| TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE |
| FILE REPERENCE: 112739-122US |
| CURRENT APPLICATION NUMBER: US/10/712,447 |
| PRIOR PILING DATE: 2003-11-13 |
| PRIOR PILING DATE: 2003-11-13 |
| PRIOR FILING DATE: 2003-11-13 |
| PRIOR PRIOR DATE: 2003-11-13 |
| PRIOR FILING DATE: 2003-11-13 |
| PRIOR PRIOR DATE: 2003-11-13 |
| PRIOR FILING DATE: 2003-11-13 |
| PRIOR FILIN
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PERTURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
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NAME/KEY: MOD_RES
LOCATION: (14)
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US-10-712-447-74

i Sequence 74, Application US/10712447

i Publication No. US20040186057A1

j Publication No. US20040186057A1

j GENERAL INFORMATION:
 APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

j APPLICANT: GARBER, DAVID W.

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT APPLICATION NUMBER: 60/425,821

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENTIN Ver. 3.2

LENGTH: 18
                                                                                                                  0; Gaps
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CRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
COTHER INFORMATION: peptide
US-10-712-447-74
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89.8%; Score 88; DB 4; Length 18;
Best Local Similarity 77.8%; Pred. No. 3.7e-06;
Matches 14; Conservative 4; Mismatches 0; Indels
                                                               Query Match

89.8%; Score 88; DB 4; Length 18;
Best Local Similarity 77.8%; Pred. No. 3.7e-06;
Matches 14; Conservative 4; Mismatches 0; Indels
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; OTHER INFORMATION: (DiMe) Lys US-10-712-447-53
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Search completed: May 19, 2006, 15:27:57 Job time: 81.2857 secs

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17, Appl 885, Appl 2, Appli 2, Appli 56, Appli 23, Appl 11, Appli 11, Appli 3, Appli 3, Appli 23, Appli 23, Appli 23, Appli 24, Appli 25, Appli 25, Appli 26, Appli

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                                                                                                                                                                                                                                                                                                                         US-11-190-750-137

US-11-204-27-1

US-10-205-928-12

US-10-505-928-859

US-11-249-111-88

US-11-249-111-88

US-11-251-738-6

US-10-505-928-569

US-11-280-997-1

US-11-280-997-2

US-11-280-997-2

US-11-280-997-25

US-11-280-997-25

US-11-280-997-25

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US-11-280-997-25

US-11-280-997-26

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US-11-280-997-25

US-11-146-700-3
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38.8%; Score 38; DB 1;
Best Local Similarity 63.6%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LRRFIGSIWRF 12
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ORGANISM: Homo sapiens
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NAME/KEY: SITE
LOCATION: (74)
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Sequence 2947, Ap
Sequence 2401, Ap
Sequence 142, App
Sequence 5, App 11
Sequence 109, App 11
Sequence 115, App 12
Sequence 115, App 13
Sequence 14, App 13
Sequence 46, App 13
Sequence 47, App 13
Sequence 14, App 13
Sequence 16, App 13
                                                                                                                                                                                                                                                                                                                                                                                     1: FEMC Celerra SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
6: /EMC Celerra SIDS3/ptodata/2/pubpaa/USI0_NEW_PUB.pep:*
7: /EMC Celerra SIDS3/ptodata/2/pubpaa/USI0_NEW_PUB.pep:*
8: /EMC Celerra SIDS3/ptodata/2/pubpaa/USI0_NEW_PUB.pep:*
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17.943 Million cell updates/sec
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Sequence 6
Sequence 3
Sequence 1
                                                                                         May 19, 2006, 15:18:37 ; Search time 2.14286 Seconds
                GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-511-937-2947

US-09-949-925-142

US-10-505-928-543

US-11-302-678-5

US-11-169-140-109

US-11-169-140-109

US-11-190-750-135

US-11-244-544-87

US-11-242-564-48

US-11-242-565-18

US-11-242-505A-18

US-11-242-505A-18

US-11-242-505A-18

US-11-311-555-16

US-11-311-555-16

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US-11-024-544A-169
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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5 FIGSIWRFIRAFYG 18
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31 FLILVWIFV-AFYG 43
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 142
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Matches 7; Conservative
                                                                     Query Match 35.7
Best Local Similarity 55.6
Matches 5; Conservative
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ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens US-10-511-937-2401
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US-09-949-925-142
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US-10-505-928-543
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APPLICANT: Prentice, James
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: Patentin Version 3.2
LENGTH: 441
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APPLICANT: Ly, Ngoc, Andes
APPLICANT: Pertitice, James
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: MUNDER: US/10/511,937
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-04-24
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR APPLICATION NUMBER: US/10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR PILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOOFTWARE PARENT NEASON NUMBER: US/10/31,831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.3%; Score 37.5; DB 6; Length 441; 33.3%; Pred. No. 11; tive 5; Mismatches 6; Indels 3
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Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
                                                                                                                                                                                             APPLICANT: EXPRESSION DIAGNOSTICS, INC
                                                                                                                     Sequence 2947, Application US/10511937 Publication No. US20060088836A1 GENERAL INFORMATION:
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APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
                                                                                                                                                                                                                                                 APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
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Best Local Similarity 33.34
Matches 7; Conservative
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     59 LREVSGKIWRF 69
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US-10-511-937-2947
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Ouery Match

Bett Local Similarity 35.4%; Score 35; DB 6; Length 651;

Bett Local Similarity 35.4%; Pred, No. 48;

Bett Local Similarity 35.4%; Pred, No. 48;

Bett Local Similarity 35.4%; Pred, No. 48;

Bett Bett Local Similarity 35.4%; Pred, No. 48;

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APPLICANT: SHERLDAN, Philip, J.
APPLICANT: SHERLDAN, Philip, J.
APPLICANT: SHERLDAN, Philip, J.
APPLICANT: HAWLEY, Stephen
APPLICANT: GLYN, Jacqueline, M.
TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CEI
TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CEI
TITLE OF INVENTION: WIMBER: US 60/267,601
FRIOR FILLING DATE: 2000-11-14
FRIOR PELICATION NUMBER: US 60/248,819
FRIOR PELICATION NUMBER: US 60/248,478
FRIOR APPLICATION NUMBER: US 60/248,478
FRIOR APPLICATION NUMBER: US 60/248,478
FRIOR PELICATION NUMBER: US 60/248,478
FRIOR PELICATION NUMBER: US 60/249,039
FRIOR FILLING DATE: 2001-10-02
FRIOR PELICATION NUMBER: US 60/248,48
FRIOR FILLING DATE: 2001-10-02
FRIOR PELICATION NUMBER: US 60/248,48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/11024544A

| Sequence 21, Application US/11024544A
| Publication No. US20060094086A1
| GENERAL INFORMATION
| APPLICANT: E.i. duPont de Nemoure and Company, Inc.
| APPLICANT: Yadav, Narendra
| APPLICANT: Xue, Zhixiong
| APPLICANT: Xue, Zhixiong
| APPLICANT: Xue, Zhixiong
| APPLICANT: Xue, Zhixiong
| TITLE OF INVENTION: DIACYLGINCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
| TITLE OF INVENTION: FATTY ACIDS AND OIL CONTENT IN OLEAGINOUS ORGANISMS
| TITLE OF INVENTION WIMBER: US/11/024,544A
| CURRENT APPLICATION WIMBER: 2004-12-29
| NUMBER OF SEQ ID NOS: 175
| SOFTWARE: Patentin version 3.3
| SEQ ID NO 21
| LENGTH: 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 7; Length 244;
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34.2%; Score 33.5; DB 7; Length 503;
Best Local Similarity 43.8%; Pred. No. 64;
Matches 7; Conservative 3; Mismatches 5; Indele
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DATABASE ENTRY DATE: 2003-10-31
RELEVANT RESIDUES: (1)..(503)
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Pred. No. 27
Sequence 109, Application US/11169140
Publication No. US20060099150A1
GENERAL INFORMATION:
APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Magnaporthe grisea 70-15
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Best Local Similarity 42.19
Matches 8; Conservative
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Pred. No. 55;
3; Mismatches
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57.1%; Pred. No. 64;
tive 3; Mismatches
  PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
SEQ ID NO 543
LENGTH: 522
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Best Local Similarity 47.1%;
Matches 8; Conservative
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US-10-505-928-543
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Best Local Similarity
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64 LGNVWRF 70
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US-11-169-140-109
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Gaps

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US-11-242-505A-48

Sequence 48, Application US/11242505A

Publication No. US20060099656A1

PUBLICATION:

APPLICANT: Carroll, Joseph M.
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156 RRFV-STWKLIALVHG 170
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50.0%;
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Best Local Similarity 62.5°
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Best Local Similarity 50.0
Matches 5; Conservative
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84 AIWRQLRDYY 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Yadar, Narendra S.
APPLICANT: Zhang, Hongxiang
APPLICANT: Zhang, Hongxiang
APPLICANT: Zhang, Hongxiang
TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
CURRENT APPLICATION NUMBER: US/11/264,784
CURRENT APPLICATION NUMBER: US/11/264,784
CURRENT APPLICATION NUMBER: 206-11-01
NUMBER OF SEQ ID NOS: 375
SOFTWARE: Patentin version 3.3
SEQ ID NO 87
LENGTH: 503
TYPE
                                                                                                        1;
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US-11-190-750-135
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34.2%; Score 33.5; DB 7; Length 503;
Best Local Similarity 43.8%; Pred. No. 64;
Matches 7; Conservative 3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 87, Application US/11264784
Publication No. US20060094052A1
FUBLICANT: E.1. duPont de Nemours & Co., Inc., APPLICANT: Bamade, Howard Glenn, APPLICANT: Damade, Howard Glenn, APPLICANT: Macool, Daniel Joseph, APPLICANT: Picataggio, Stephen K., APPLICANT: Pollark, Dana M. Walters, APPLICANT: Regghianti, James John APPLICANT: Ragghianti, James John APPLICANT: Rue, Zhixiong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 34.2%; Score 33.5; D
Best Local Similarity 43.8%; Pred. No. 64;
Matches 7; Conservative 3; Mismatches
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156 RRFV-STWKLIALVHG 170
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 3 RRFIGSIWRFIRAFYG 18
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OTHER INFORMATION: DGAT1
US-11-264-784-87
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APPLICANT: Callot, Cospin in.
APPLICANT: Healy, Alleen
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: 14355, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310, c
FILE REFERENCE: MPIZO01-288PIRCPIONNIM
CURRENT FILING DATE: 2005-10-03
PRIOR APPLICATION NUMBER: US 10/290,078
PRIOR APPLICATION NUMBER: US 60/347,949
PRIOR PILING DATE: 2001-11-07
PRIOR PELING DATE: 2001-11-07
PRIOR FILING DATE: 2001-12-16
PRIOR FILING DATE: 2001-12-16
PRIOR FILING DATE: 2001-12-17
PRIOR FILING DATE: 2001-12-17
PRIOR FILING DATE: 2001-12-17
PRIOR FILING DATE: 2001-12-17
PRIOR SEQ ID NOS: 48
SOFTWARE PRESENCE FOR Windows Version 4.0
FUNDER OF SEQ ID NOS: 48
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Pred. No. 50;
3; Mismatches 2; Indels
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| Sequence 7, Application US/11204427
| Publication No. US20060100146A1
| GENERAL INFORMATION:
| APPLICANT: Sturley, Stephen L
| APPLICANT: Turkish, Aaron R
| APPLICANT: Turkish, Aaron R
| APPLICANT: Cromley, Debra
| TITLE OF INVENTION: AWAT-RELATED METHODS AND ARTICLES
| TITLE OF INVENTION: AWAT-RELATED METHODS
| CURRENT APPLICANION NUMBER: US/11/204,427
| CURRENT APPLICANION NUMBER: US/11/204,427
| UNMERR OF SEQ ID NOS: 73
| SEQ ID NO 7
| LENGTH 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 7;
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Pred. No.
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Query Match
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Sequence 46, Application US/11304129

Publication No. US20060088915A1

GENERAL INFORMATION:
APPLICANT: OHTAKI, Tetsuya

APPLICANT: HATATSU, Yoshihiro
APPLICANT: HATANA, Yasushi
APPLICANT: HATANA, Yasushi
APPLICANT: HATANA, Yasushi
APPLICANT: HATANA, Yasushi
APPLICANT: HATANA, Syuji
I TILE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
FILE REFERENCE: 2762US0P
CURRENT APPLICATION NUMBER: US/11/3304,129
FRIOR FILING DATE: 2003-09-29
FRIOR FILING DATE: 2000-07-18
FRIOR FILING DATE: 2001-02-02
FRIOR FILING DATE: 2001-02-02
FRIOR FILING DATE: 2001-07-18
FRIOR FILING DATE: 2001-07-18
FRIOR FILING DATE: 2001-07-18
FRIOR FILING DATE: 2001-07-18
FRIOR FILING DATE: 2001-07-17
                                                                                             APPLICANT: MASUDA, Yasushi
APPLICANT: MASUDA, Yasushi
APPLICANT: TAKATSU, Yoshihiro
APPLICANT: TAKATSU, Yoshihiro
APPLICANT: TERAO, Yasushi
APPLICANT: HINNAM, Saushi
APPLICANT: HINUAM, Syuji
ITILE OF INVERTION: Novel Physiologically Active Peptide and Use Thereof
FILE REFERENCE: 2762USOP
CURRENT APPLICATION NUMBER: US/11/304,129
CURRENT FILING DATE: 2003-09-29
FRIOR APPLICATION NUMBER: US/10/333,192
FRIOR APPLICATION NUMBER: US/200-217442
FRIOR APPLICATION NUMBER: JP 2000-217442
FRIOR FILING DATE: 2001-02-02
FRIOR FILING DATE: 2001-02-03
FRIOR FILING DATE: 2001-02-03
FRIOR FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 58
SEQ ID NO 40
LENGTH: 393
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Pred. No. 58;
1; Mismatches 6; Indels
Sequence 40, Application US/11304129
Publication No. US20060088915A1
APPLICANT: OHTAKI, Tetsuya
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Best Local Similarity
Local 6; Conserve
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Best Local Similarity
Matches 6; Conserv
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US-11-304-129-40
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APPLICANT: Carroll, Joseph M.
APPLICANT: Healy, Aileen
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 14717, 9941, 19310, c
TITLE OF INVENTION: Hematological Disorders Using 232, 205, 10630, 14717, 9941, 19310, c
TITLE OF INVENTION: Hematological Disorders Using 232, 205, 10630, 14717, 9941, 19310, c
TITLE OF INVENTION: MIMBER: US/11/242,505A
CURRENT PRILING DATE: 2005-10-03
PRIOR FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: US 10/320,351
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 48
SEQ ID NO 18
LENGTH: 403
LENGTH: 403
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                                                                                                                                                                   US-11-242-505A-18
; Sequence 18, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
                                                     216 FCGQIWPVDQQFY 228
5 FIGSIWRFIRAFY 17
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155 VRRVLGAVW 163
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 4; Conserv
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Synthetic Synthetic Synthetic

Synthetic

Lecithin:

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a composition and an encoding an monoclonal antibody that specifically binds to the synthetic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina, low-density lipoprotein; LDL; very low density lipoprotein; UDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
                                                       Ado34245 | Ado34210 | Ado34310 | Ado343118 | Ado34310 | Ado34242 | Ado34211 | Ado34212 | Ado34312 | Ado34313 | Ado34332 | Ado34333 | Ado34326 | Ado34333 | Ado34326 | Ado34333 | Ado34326 | Ado34333 | Ado34326 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117.
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                                                       ADO34245
ADO34301
ADO34314
ADO34318
ADO34302
ADO34303
ADO34303
ADO34303
ADO34313
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ADO34320
AAY18917
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                             AD034239
                                           ADO34319
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                                                                                                    Garber
   (UABR-) UAB RES FOUND
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WO2004043403-A2
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   ADO34340;
   Synthetic
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87.287 Million cell updates/sec
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               GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Maximum DB seq length: 200000000
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apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for trading coronary artery disease, gyocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein-E mimicking to polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E 8×6666666666666688&

Sequence 18 AA;

Gaps ö 100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 3.9e-08; 0; Indels 0; Mismatches 1 GIRRFIGSIWRFLRAFYG 18 1 GIRRFIGSIWRFLRAFYG 18 Best Local Similarity 100. Matches 18; Conservative Query Match ઠ

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ADO34231 standard; peptide; 18 AA ADO34231; 

(first entry) 12-AUG-2004 Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 8.

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasctropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

Synthetic

WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND.

Anantharamiah GM, Garber DW,

ö Datta

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 8; 79pp; English

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

cardiant, vasofropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E minicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E minicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VDDL) to a cell and enhances degradation of LDL or very low very low construction of the subject and construction of the construction of LDL by a cell. This sequence represents a synthetic apolipoprotein-E ö Gaps mimicking polypeptide has the following activities: antilipaemic, .. 0 Score 94; DB 8; Length 18; Pred. No. 1.6e-07; 2; Mismatches 0; Indels mimicking polypeptide of the invention. ADO34354 standard; peptide; 18 AA. 1 GIRRFLGSIWRFIRAFYG 18 1 GIRRFIGSIWRFLRAFYG 18 95.9%; 12-AUG-2004 (first entry) Query Match Best Local Similarity 88.9° Matches 16; Conservative Sequence 18 AA; AD034354; ADO34354 ID ADO3 RESULT 3 8888888888888888888888888 셤 à

apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL. Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 131. 

Synthetic.

WO2004043403-A2

27-MAY-2004.

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P.

(UABR-) UAB RES FOUND

WPI; 2004-411629/38.

Anantharamiah GM,

ö

Datta

Garber DW,

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 131; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic,

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cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is such is for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalioporteinaemia or atheroscalcaosis, and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or winding wimicking polypeptide of the invention.
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Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide. apolipoprotein-E mimicking polypeptide, antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia, atherosclerosis; myocardial infarction; siroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDDL. ADO34225 standard; peptide; 18 AA (first entry) 12-AUG-2004 ADO34225; 

'note= "N-terminal acetyl" /note= "C-terminal amide" Location/Qualifiers Key Modified-site Modified-site Synthetic

MO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P.

(UABR-) UAB RES FOUND

Anantharamiah GM, Garber DW, Datta G WPI; 2004-411629/38. Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. Claim 4; SEQ ID NO 2; 79pp; English. The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E

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cc the synthetic apolypeptide encoding polynuclectide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and can monocolonal antibody that specifically binds to the synthetic apolipoprotein-E amicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosolerotic, cerebroprotective, and cardiant, vasotropic, antiarteriosolerotic, cerebroprotective, and cardiant, vasotropic, antiarteriosolerotic, cerebroprotective, and cardiant, reducing serum cholesterol in a subject (including a mammal cuseful for reducing serum cholesterol in a subject (including a mammal confingment or or angulatiant); for treating coronary artery disease, dysbetalipoproteineemia or atherosclerosis, and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (VLDE) to a cell and enhances degradation of LDE or VLDE by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL;
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                                                                                                                                                                                                                                                                                                                                                                                                                          95.9%; Score 94; DB 8; Length 18; 88.9%; Pred. No. 1.6e-07;
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 AA;
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the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is untianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, chimpanzee or orangutan) for treating coronary artery disease, and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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   Score 94; DB 8; Length 18;
Pred. No. 1.6e-07;
2; Mismatches 0; Indels
                               7
                                                            1 GIRRFIGSIWRFLRAFYG 18
    95.9%;
88.9%;
Ouery Match
Best Local Similarity 88.9
Matches 16, Conservative
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Gaps

윱 ADO34352 standard, peptide; 18 AA. 

12-AUG-2004 (first entry)

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 129.

apolipoprotein-E mimicking polypeptide, antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease, dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; seroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; LDL; very low density lipoprotein; VLDL.

Synthetic

WO2004043403-A2.

27-MAY-2004

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

Datta G; Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 129; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polygeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic

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              an innocuriant authory that a population is a minimal and in a minimal cking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerboroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholopoprotein-E mimicking polypeptide is useful for reducing serum cholopoprotein-E mimicking polypeptide is useful for reducing serum cholopoprotein-E mimicking polypeptide is such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein [UDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary arrery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VDL.
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monoclonal antibody that specifically binds to the synthetic
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Pred. No. 1.6e-07;
2; Mismatches 0; Indels
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apolipoprotein-B mimicking polypeptide. The synthetic apolipoprotein-B mimicking polypeptide has the following activities: antilipaemic, cardiant, vasokropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apollipoprotein-B mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanize or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-B mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or will by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
                    888888888888888888888888
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; Score 94; DB 8; Lengtn 10, Pred. No. 1.6e-07; 2; 1 GIRRFIGSIWRFLRAFYG 18 95.9%; Query Match
Best Local Similarity
Local Similarity
Local 16;
Conservative 8

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Gaps

RESULT 8 ADO34236

ADO34236 standard; peptide; 18 AA. ADO34236; Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 13.

(first entry)

12-AUG-2004

vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL. apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; 

Synthetic

WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

Datta G; Garber DW, Anantharamiah GM,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 13; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymucleotide, a composition comprising mimicking polypeptide and a composition comprising an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

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         cardiant, vasotropic, antiarteriosclerdic, cerebroportective, and antianginal. The synthetic apolipoprotein-E minicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of myocardial infarction or atherosclerosis; and for reducing the subject; myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E minicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or minicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDL.
                                                                                                                                                                                                                                                                              Gaps
mimicking polypeptide has the followind activities: antilipaemic,
                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116.
                                                                                                                                                                                                                                            Score 94; DB 8; Length 18; Pred. No. 1.6e-07; 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                             1 GIRRFLGSIWRFIRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                     ADO34339 standard; peptide; 18
                                                                                                                                                                                                                                                                                                             18
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                                                                                                                                                                                                                                                95.98;
                                                                                                                                                                                                                                                                                                             1 GIRRFIGSIWRFLRAFYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                16; Conservative
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                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anantharamiah GM,
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                                                                                                                                                                                                                   Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADO34339;
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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transpensio, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence. Claim 4; SEQ ID NO 116; 79pp; English. WPI; 2004-411629/38.

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antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, dimpanzee or orangutan); for treating coronary artery disease, myocardial infarction or atherosclerosis, and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein-E mimicking oblypeptide enhances binding of low-density lipoprotein (ULD) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking mimicking polypeptide of the invention.
cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
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0; Indels
     Score 94; DB 8; I Pred. No. 1.6e-07;
                              2; Mismatches
                                                       1 GIRRFIGSIWRFLRAFYG 18
     95.9%;
Query Match
Best Local Similarity 88.9
Matches 16; Conservative
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Gaps

.; 0

Length 18;

1 GLRRFIGSIWRFIRAFYG 18

ADO34233 standard; peptide; 18 AA (first entry) 12-AUG-2004 AD034233; RESULT 10 AD034233 

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 10.

apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholestron; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

WO2004043403-A2.

27-MAY-2004

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P.

UABR-) UAB RES FOUND

Datta G; Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 10; 79pp; English

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide enroding polymucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic and apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polymucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide and acarrier; and an mimicking polypeptide has the following activities: antilipaemic, cardiant, vasotropic, antiatteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

Claim 4; SEQ ID NO 127; 79pp; English.

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antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rate, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or winmicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dybeteralipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant;
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                                                                                                                                                                                                              Score 94; DB 8; Length 18;
Pred. No. 1.6e-07;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Datta G;
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                                                                                                                                                                                                                 95.9%;
                                                                                                                                                                                                                                                                              1 GIRRFIGSIWRFLRAFYG
                                                                                                                                                                                                                                                                                              1 GIRRFLGSIWRFIRAFYG
                                                                                                                                                                                                           Query Match
Best Local Similarity 88.9
                                                                                                                                                                                                                                                                                                                                                                                                                                              12-AUG-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anantharamiah GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004043403-A2.
                                                                                                                                                                                       Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                  ADO34350;
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useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apollpoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (UDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or WLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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                                    Gaps
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           Score 94; DB 8; Length 18;
Pred. No. 1.6e-07;
                                    2; Mismatches
                                                                                  GLRRFIGSLWRFLRAFYG 18
                                                           1 GIRRFIGSIWRFLRAFYG 18
           95.9%;
Query Match
Best Local Similarity 88.2
Best Local Similarity
Best Local Similarity
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ADO34314 standard; peptide; 18 AA. 12-AUG-2004 (first entry) AD034314; RESULT 12 ADO34314 

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 91.

apolipoprotein-E mimicking polypeptide, antilipaemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, antianginal, serum cholesterol, coronary artery disease, dysbetalipoproteinaemia, atherosclerosis, myocardial infarction, stroke, embolus, angina, low-density lipoprotein, LDL, very low density lipoprotein; UDL.

Synthetic.

WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

ö Datta Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 91; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide acomposition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antipody that specifically binds to the synthetic apolipoprotein-E apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E arimicking polypeptide. The synthetic apolipoprotein-E cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antiandinal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal

such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

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      chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (UDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel synthatic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-C ardiant, vasotropic, antiatreriosofleroric, cerebroprotective, and antiandinal. The synthetic apolipoprotein-E mimicking serum cholesterol in a subject (including a mammal useful for reducing serum cholesterol in a subject (including a mammal manke).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
                                                                                                                                                                                                                                                                               Gaps
such as a mouse, rat, rabbit, cow, shedp, pig, human, monkey, ape,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 74.
                                                                                                                                                                                                                                     Score 91, DB 8, Length 18;
Pred. No. 4.8e-07;
3, Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADO34297 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                              1 GIRRFIGSIWRFLRAFYG
                                                                                                                                                                                                                                         95.98;
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                                                                                                                                                                                                                                                                                 15; Conservative
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Best Local Similarity
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                                                                                                                                                                                                   Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AD034297;
                                                                                                                                                                                                                                                                                   Matches
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chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinsemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; bor breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or WLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
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Gaps
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Length 18;
89.8%; Score 88; DB 8; Lei
77.8%; Pred. No. 1.4e-06;
iive 4; Mismatches 0;
                                                      1 GIRRFIGSIWRFLRAFYG 18
                                                                              18
                             Conservative
            Local Similarity
les 14; Conserv
  Query Match
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ADO34244 standard; peptide; 18 (first entry) 12-AUG-2004 ADO34244; 

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Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 21.

apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; UDL;

Synthetic

WO2004043403-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P

(UABR-) UAB RES FOUND

Ö Anantharamiah GM, Garber DW,

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 21; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polyapptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein. E mimicking polyapptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polyapptide encoding polympetide, a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that the following activities: antilipaemic, cardiant, vasotropic, antiarreriosclerotic, cerebroprotective, and antiarginal. The synthetic apolipoprotein-E mimicking polypeptide is antiarreriosclerotic, cerebroprotective, and antiarginal. The synthetic apolipoprotein-E mimicking polypeptide is such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease,

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide, a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polypeptide a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide and a carrier; and apolipoprotein-E mimicking polypeptide and a carrier; cardiant, vasotropic, antiatteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

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            myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (UDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.
dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  apolipoprotein-E mimicking polypeptide; antilipaemic; cardiant; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinaemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.
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/note= "All Lys residues are DiMethyl-Lysine"
                                                                                                                                                                                                                                                                                                                                                                                         Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 53.
                                                                                                                               Score 88; DB 8; Lengtn 10, Pred. No. 1.48-06;
                                                                                                                                                                        4; Mismatches
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                                                                                                                                                                                                                                                                                                       ADO34276 standard; peptide; 18 AA.
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1 GIRRFLGAIWRFIRSFYG 18
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                                                                                                                                           89.8%;
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                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                         Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UABR-) UAB RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-411629/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anantharamiah GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004043403-A2
                                                                                                                Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                     ADO34276;
                                                                                                                                              Query Match
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useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, dyshetalipoer or cangutan); for treating coronary artery disease, or any and also for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject, and also for treating angina. The synthetic apolipoprotein. E mimicking apolypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein. E mimicking mimicking polypeptide of the invention.
               888888888888888
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0 Gaps ö Query Match

89.8%; Score 88; DB 8; Length 18;
Best Local Similarity 77.8%; Pred. No. 1.4e-06;
Matches 14; Conservative 4; Mismatches 0; Indels Length 18;

1 GIRRFIGSIWRFLRAFYG 18 ||:||:||:||||| 1 GIKRFLGSIWRFIKAFYG 18

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Search completed: May 19, 2006, 14:24:30 Job time: 94.2857 sec8

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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May 19, 2006, 14:24:57 ; Search time 14.2857 Seconds (without alignments) 121.233 Million cell updates/sec Run on:

1 GIRRFIGSIWRFLRAFYG 18 US-10-712-447-117 98 Title: Perfect score: Sequence:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**:**:-

## SUMMARIES

Ouery Match 19.0	Len	h DB	ID S76462 B84733	riptic  thetic able c
o o .	489	0 0	B84733 I54412	HLA-A ce
ن ن	- 6	23	HLHU69 HLHUA2	MHC Class I nistoc MHC class I histoc
46.9	10.10	2 2	I38443 I61902	gene HLA-A-0203 pr MHC class I histoc
0		2	137542	class I
46.9 36		20 1	I84448	MHC class I histoc
. 6.		. ro	138442	gene HLA-A-0205 pr
•		6 2	T33269	hypothetical prote
45.9 519		6	T02263	cytochrome P450 DW
45.9 719		N N	AG3325 E84953	DNA 11gase (NAD) ( penicillin-binding
44.9 589		•••	A34341	poly (3-hydroxybuty
0.0			A84060	leucyl-tRNA synthe
44.4 790	70	N N	T50337	homolog to drosoph
٥.		•	A75578	transcription regu
4		•	AH3568	981
٥.		2	C42595	
o		••	B90410	hypothetical prote
42.9 803		•••	AD1282	
o.		• •	AH1653	S)
۳.		•	T19064	
41.8 13		1 2	AG2115	hypothetical prote
41.8 207			D84114	ltra
41.8 27		2	S21348	probable pot polyp

ABC-type sugar tra hypothetical prote	hypothetical proce probable sodium-tr hypothetical proce leucyl-rRNA synthe	ND5 intron 4 prote probable transcrip hypothetical prote	hypothetical prote hypothetical prote hypothetical prote	hypothetical prote probable permease hypothetical prote	transporter, mfs s
E97350 T08940	F965/1 B81690 T04745 B89961	S09145 T52113 B84023	G64032 T15530 F64642	B72692 F82993 AF2320	AD3417
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384	503 537 804	1003 107 127	139 228 231	237 374 411	418
41.8	4 4 4 4 1 1 4 1 4 8 6 6 1 1 8	41.8 40.8 40.8	40.8 40.8	40.8 8.04	40.8
41	4 4 4 4 1 11 11 11	4 4 4 1 0 0	4 4 4 0 0 0	0 4 4 0 0 0	40
30	W W W W W W A W	33.3 87.8	39 4 4 0 1 0	4 4 4 2 & 4	45

## ALIGNMENTS

	RESULT 1	
	S76462	
	hypothetical protei	hypothetical protein - Synechocystis sp. (strain PCC 6803)
	C; Species: Synechocystis sp.	cystis sp.
	A, Variety: PCC 6803	E
	C; Date: 25-Apr-1997	C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
٠	C,Accession: S76462	
	R; Kaneko, T.; Sato,	R, Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Mıyajıma, N.;
	o, K.; Okumura, S.	; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
	DNA Res. 3, 109-136	6, 1996
	A; Title: Sequence &	A, Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
	8.	
	A;Reference number	A;Reference number: S74322; MUID:97061201; PMID:8905231
	A; Accession: S76462	
	A;Status: preliminary	ary
_	A; Molecule type: DNA	NA
	A, Residues: 1-627 < KAN>	<kan></kan>
	A, Cross-references	A, Cross-references: UNIPROT: P74489; UNIPARC: UP100000C103F; EMBL: D90915; GB: AB001339; NID:
	A, Note: the nucleot	A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
	Ouery Match	Ouery Match 49.0%; Score 48; DB 2; Length 627;
	Best Local Simil	arity 38.9%; Pred. No. 8;
	Matches 7; Co	7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
	Oy 1 GIRRI	1 GIRRFIGSIWRFLRAFYG 18
	••	
	DP 597 GLEQI	597 GLEQLLGKIWQWLRQKFG 614

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48.0%; Score 47; DB 2; Length 489; Query Match

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Conservative

Best Local Similarity Matches 8; Conserv

6 IGSIWRFLRAF 16

64

||::| ||||| 54 IGNMWSFLRAF

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Fixence: 11205-1210, 1985

EMBO J. 4, 1205-1210, 1985

EMBO J. 4, 1205-1210, 1985

A,7Title: Unusual RNA splicing generates a secreted form of HLA-A2 in a mutagenized B lymg A,7Title: Unusual RNA splicing generates a secreted form of HLA-A2 in a mutagenized B lymg A,7EGERION: A02191

A,ACCESSION: A02191

A,Residues: 39-365 <KRA-
A,CRAS-references: UNIPARC:UPI000016AA56; GB:X02457; NID:g32153; PIDN:CAA26297.1; PID:g3

A,Residues: 39-365 <KRA-
B,Residues: 39-365 <KRA-
A,FORDE: the author translated the codon CAG for residue 96 as His, ACU for residue 97 as B Thr, and ACU for residue 323 as Ser
R,Casteno, A.R.; Lopez de Castro, J.A.
Immunogenetics 34, 281-285, 1991

A,7Title: Structure of the HLA-A*0204 antigen, found in South American Indians. Spatial c)
A,7Eference number: S19020; MUID:92039809; PMID:1937577
C;Date: 28-Feb-1980 #sequence revision 22-Apr-1995 #text change 08-Dec-2000 C;Accession: I55948; B35997; $\tilde{A}\) $02191; $19020; $77965; $23\) $23\) $3834; $A93919; $14802; $A021 R;Koller, B.H.; Orr, H.T. Ur. Immunol. 134, 2727-2733, 1985 A;Title: Cloning and complete sequence of an HLA-A2 gene: Analysis of two HLA-A alleles a A;Reference number: I55948; WUD:85132727; PMID:2982951
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPARC:UPI0000124E24; GB:K02883; NID:g187605; PIDN:AAA98727.1; PID:ç A;Experimental source: lymphoblastoid cell line 721
R;Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P. Proc. Natl. Acad. Sci. U.S.A. 87, 2833-2837, 1990
A;Title: Rapid cloning of HLA-A,B cDNA by using the polymerase chain reaction: frequency A;Reference number: A35997; MUID:90207291; PMID:2320591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Modecule type: protein
A; Residues: 25-55, Z',57-60, B',62, B',64-66, Z',68-74, X',76-85, RXXX',90-94, AH',97,'V'
A; Cross-references: UNIPARC:UPI00001737EE
A; Note: this sequence has been revised in reference A93919
R; Lopez de Castro, J.A.; Strominger, J.L.; Strong, D.M.; Orr, H.T.
Proc. Natl. Acad. Sci. U.S.A. 79, 3813-3817, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residuss: 1.365 <BEL>
A;Cross-references: UNIPARC:UPI0000124E24; EMBL:M84379; NID:g403143; PIDN:AAA59606.1; PII
A;Experimental source: cell line GRC 138; isolate A*0201
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ricastano, A.R.; Lopez de Castro, J.A.
Immunogenetics 35, 344-346, 1992
A;Title: Structure of the HLA-A *0211 (A2.5) subtype: further evidence for selection-driv
A;Reference number: S23593; WUID:92218010; FMID:1559719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PID:
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A;Note: this allele is designated A*0201 (previously HLA-A2.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A/Status: preliminary
A/Status: preliminary
A/Molecule type: mRNA
A/Molecule type: mIndepart this mallele is designated A+0204
A/Molecule mallele in two tribes of Brazilian Indians.
A/Molecule mumber: 137120; MUID:92269955; PMID:1317015
A/Accession: S77965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: S22593
A;Molecule type: mRNA
A;Residues: 9-96,'ID', 9-365 <CAS2>
A;Residues: 9-96,'ID', 9-365 <CAS2>
A;Residues: 9-96,'ID', 9-365 <CAS2>
A;Coss-references: UNIPARC:UPIO00008AF57; EMBL:X60764; NID:g32156; PIDN:CAB56609.1; P:A;Note: this allele is designated A*0211 (previously HLA-A2.5)
B;Note: this allele is designated A*0211 (previously HLA-A2.5)
R;Orr, H.T.; Lopez de Castro, J.A.; Parham, P.; Ploegh, H.L.; Strominger, J.L.
A;Orr, H.T.; Lopez de Castro, J.A.; Parham, P.; Ploegh, H.L.; Strominger, J.L.
A;Title: Comparison of amino acid sequences of two human histocompatibility antigens, JA;Reference number: A93834; MUID:80056745; PMID:92029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: nucleic acid sequence not shown, translation not shown
                                                                                                                                                                                                                                                                                                                 A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-365 <KOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-365 < ENN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S19020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: I54412
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Aclecule type: mRNA
A;Residues: 1-246 < RES>
A;Cross-references: UNIPROT:029945; UNIPARC:UPI000008A27D; GB:M27537; NID:g187727; PIDN:C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: surface antigen
F;101-166/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLHUA2
MHC class I histocompatibility antigen HLA-A2 alpha chain precursor [validated] - human
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: 154412
R; Arnot, D.; Lillie, J.W.; Auffray, C.; Kappes, D.; Strominger, J.L.
Immunogenetics 20, 237-252, 1984
A; Title: Inter-locus and intra-allelic polymorphisms of HLA class I antigen gene mRNA.
A; Reference number: 154412; MUID: 84287690; PMID: 6332068
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F;85/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: B24671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
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                                                               Indels
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EMBO J. 4, 2849-2854, 198
A;Title: Exon shuffling in vivo can generate novel HLA c
A;Reference number: A91021; MUID:86055720; PMID:3877632
                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 2;
Pred. No. 6.7;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MHC HLA-A cell surface antigen - human (fragment)
                      Pred. No. 9;
2; Mismatches
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46.9%; ilarity 58.3%; Conservative

Query Match Best Local Similarity Matches 7; Conserv

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C,Genetics: A,Gene: GDB:HLA-A A,Cross-references: GDB:119310; OMIM:142800

A; Molecule type: DNA A; Residues: 1-273 <HOL> A;Accession: B24671

A;Map position: 6p21.3-6p21.3 A;Introns: 89/3

VĠSDWŔFĽŔGYH 113

RESULT 5

Conservative 6 IGSIWRFLRAFY 17

Local Similarity les 7; Conserv

Query Match Best Loc Matches ო

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MHC class I histocompatibility antigen HLA-A2 alpha chain (allele A*0216) precursor - hun C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000 C; Accession: 137542; S4958; S4958 F. Bodmer, J.; Browning, M.J.; McMichael, A.J. Immunogenetics 41, 388, 1995 A; Fittle: Identification of a novel HLA-A2 subtype, HLA-A*0216.
A; Reference number: 137542; MUID:95278976; PMID:7759139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CjAccession: 184448
R;Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; I Nature 357, 326-329, 1992
A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.
A;Reference number: 137120; MUID:92269955; PMID:1317015
                                                                                                           C;Accession: 161902
R;Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; I
Nature 357, 326-329, 1992
A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.
A;Reference number: 137120; MUID:92269955; PMID:1317015
A;Accession: 161902
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F;I-24/Domain: signal sequence #stocaus predicted <SIG>
F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predic
F;220-285/Domain: immunoglobulin homology <IMM>
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A;Cross-references: UNIPARC:UPI000016AA63; BMBL:246633; NID:9575248; PIDN:CAA86602.1; PII
A;Note: submitted to the EMBL Data Library, November 1994
                                                                                                                                                                                                                                                                                                                                                                                                   A,Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Foredidues: 1-365 - FRES>
A,Status: UNIPARC:UPI000016AD39; GB:M84378; NID:g187625; PIDN:AAAS9604.1; PID:gA,Experimental source: cell line KRC 033; isolate A*0212
                                                                       06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 23-Jul-1999
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A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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Pred. No. 9.8;
3; Mismatches
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A,Molecule type: mRNA
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3; Mismatches
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58.3%;
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Matches 7; Conservative
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127 VGSDWRFLRGYH 138
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127 VGSDWRFLRGYH 138
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A/Map position: 6p21.3-6p21.3
A/map position: 6p21.3
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A;Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A2 A;Reference number: 138441; MUID:87252273; PMID:3496393
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MHC class I histocompatibility antigen HLA-A alpha chain precursor - human (isolate A*02
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A;Reference number: A93919; MUID:82247941; PMID:6179086
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Reference number: S14802; MUID:91204056; PMID:2017257
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A;Residues: 25-85, RXXXX, 90-94, AH', 97, 'V', 99-112, 'Z', 114-118, 'LZ', 121-125, 'X', 127-131, 232-265, 'E', 267-294 <LOP>
232-265, 'E', 267-294 <LOP>
7. Cross-reference: UNIPARC: UP100001737EF
R;Silver, M.L.; Parker, K.C.; Wiley, D.C.
Nature 350, 619-622, 1991
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
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58.3%; Pred. No. 9.8;
tive 3; Mismatches 2; Indels
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A;Molecule type: DNA
A;Residues: 1-365 <RES>
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A;Residues: 25-36 <SIL>
A;Cross-references: UNIPARC:UPI00001737F0
C;Genetics:
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127 VGSDWRFLRGYH 138
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A;Variety: isolate A*0212
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R;Winkler, R.G., Helentjaris, T.
Plant Cell 7, 1307-1317, 1995
A;Title: The maize dwarf3 gene encodes a cytochrome P450-mediated early step in gibberell
A;Reference number: 214648; MUID:96004534; PMID:7549486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:076442; UNIPARC:UPI000007D477; EMBL:AF068709; PIDN:AAC19257.J A;Experimental source: strain Bristol N2; clone C24B9
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A;Experimental source: strain B73
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C;Superfamily: Synchrocystis cytochrome P450 slr0574; cytochrome P450 homology
C;Keywords: oxidoreductase
F;325-488/Domain: cytochrome P450 homology <P45>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytochrome P450 DWARF3 - maize
N;Contains: oxidoreductase (EC 1.....)
C;Species: Zea mays (maize)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                   hypothetical protein C24B9.13 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-0c1-1999 #sequence_revision 29-0ct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AG3325
DNA ligase (NAD) (EC 6.5.1.2) [imported] - Brucella melitensis (strain 16M)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Description: involved in an early step in gibberellin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                     RiMurray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D. submitted to the EMBL Data Library, May 1998
A; Description: The sequence of C. elegans cosmid C2489, A; Reference number: Z21310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: T02263
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                          A,Accession: T33269
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 5
A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB
Pred. No. 20;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :: || |:| |: || |
252 LKFFITSLWMFMHAFDG 268
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Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
                                 :|| ||||| ::
127 VGSDWRFLRGYH 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 IGSIWRFLRAF 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-519 <WIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-516 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Genetics:
A,Gene: CESP:C24B9.13
                                                                                                                                                                                                                                                   C, Accession: T33269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
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J. Immunol. 139, 936-941, 1987
A.Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A2
A.Reference number: 138441; MUID:87252273; PMID:3496393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: UNIPROT: P01892; UNIPARC: UP1000016A06D; EMBL: U03862; NID: 912436; PID Superfamily: class I histocompatibility antigen; immunoglobulin homology < IMM>
                                                                   F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predi
F;220-285/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNÅ
A;Residues: 1-365 <RES.
A;Cross-references: UNIPROT:PO1892; UNIPARC:UPI000016AD48; GB:M24042; NID:g187777; PIDN:
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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46.9%; Score 46; DB 2; Length 365;
Best Local Similarity 58.3%; Pred. No. 9.8;
Matches 7; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                          46.9%; Score 46; DB 2; Length 365; 58.3%; Pred. No. 9.8; 2; Indels iive 3; Mismatches 2; Indels
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Pred. No. 9.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Diversity and diversification of HLA-A,B,C alleles. A;Reference number: 136956; MUID:89235215; PMID:2715640 A;Accession: I61857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D. J. Immunol. 142, 3937-3950, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
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                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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R.DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                    A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-719 cKUR>
A,Residues: 1-719 cKUR>
A,Cross-references: UNIPROT: QBYIS6; UNIPARC: UPI0000057D37; GB:AE008917; PIDN:AAL51770.1,
A,Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cjaccession: E84953
R;Shigemobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
R;Lutze 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: E84953
A;Accession: E84953
A;Cession: E84953
A;Cession: E84953
A;Cession: E84953
A;Cession: E84953
A;Cession: E84953
A;Cession: E84953
A;Residues: 1-760
A;Cross-references: UNIPARC:UPI00005E4C8; GB:AP000398; GSPDB:GN00144
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C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 31-Dec-2004
C;Accession: AG3325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
45.9%; Score 45; DB 2; Length 719;
Best Local Similarity 58.3%; Pred. No. 27;
Matches 7; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
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45.4%; Score 44.5; D
Best Local Similarity 50.0%; Pred. No. 35;
Matches 9; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Genetics:
A,Gene: mrcB; BU200
C,Superfamily: penicillin-binding protein 1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: I
C;Superfamily: DNA ligase (NAD), LigA type
C;Keywords: ligase
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102 VRDFVGSVYRFL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 IRRFIGSIWRFL 13
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sapien sapien

aspergillus

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QSaus5 QSnpg9 Q9tng7 07ynx8

homo

sapien sapien

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database

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de Kort C.A.D., Koopmanschap A.B.;

de Kort C.A.D., Koopmanschap A.B.;

"Nucleotide and deduced amino acid sequence of a cDNA clone encoding
diapause protein 1, an amylphorin-type storage hexamer of the Colorado
potato beetle.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Length 670;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P04233; ILLI.

G0; G0:0063344; F:oxygen transporter activity; IEA.
G0; G0:006310; P:transport; IEA.
InterPro; IPR000896; Hemocyanin.
InterPro; IPR005203; Hemocyanin.
InterPro; IPR005203; Hemocyanin.
PANTHER, PTHR11511; Hemocyanin.
Pfam; PF03723; Hemocyanin.
Pfam; PF03723; Hemocyanin.
Pfam; PF03722; Hemocyanin.
Pfam; PF03723; Hemocyanin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leptinotarsa decemlineata (Colorado potato beetle).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996, integrated into UniProtKB/TrEMBL 01-NOV-1996, sequence version 1. 07-FEB-2006, entry version 25. Diapause protein 1 (Fragment).
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50.0%; Pred. No. 4.3;
tive 5; Mismatches
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PROSITE; PS00210; HEMOCYANIN_2; UNKNOWN_1.
                            05NPG9<sup>2</sup>ZYMMO
09TNO7 HUWAN
07TNY1 HUWAN
06SNB2 HUWAN
040YZ9<sup>2</sup>HUWAN
040YZ9<sup>2</sup>HUWAN
070YZ9<sup>2</sup>HUWAN
070FC8<sup>2</sup>HUWAN
070FC8<sup>2</sup>HUWAN
070FC8<sup>2</sup>HUWAN
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01952C HUWAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X76080; CAA53691.1; -; mRNA.
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351 RKFYGALWSYLRHFFG 366
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Q3APYS CHLCH
ID Q3APYS_CHLCH PRELIMINARY;
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8; Conservative
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   NCBI_TaxID=7539;
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O7w193 bordetella

O7W193 pordetella

O4564 burkholderi

O4564 burkholderi

O4564 mus musculu

O4567 mus musculu

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O4569 a arabidopsis
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Q3apy5 chlorobium
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                                   GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2849598 segs, 925015592 residues
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Q3APYS CHLCH
Q84ZW1 PEA
Q9F7V7 RHILV
Q2NUBS SODGL
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XKR7 PAWIR
XKR7 MAI — MOUSE
XKR7 RAI — O7VV93 BORPE
Q7W193 BORPE
Q7W193 BORPE
Q9 9157 BURS
Q4 11M7 9 BURK
Q5 VRM7 ORYSA
Q2 11M7 9 BURK
Q6 NS 64 7 MOUSE
Q4 4 Q9 1 CHILI
Q4 4 Q9 CHILI
Q4 3 XM1 9 CHILI
Q6 3 XM1 CHILI
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Q6 G8 SE 7 CHILI
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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NCBI_TaxID=387;
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Q9F7V7_RH
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pisum sativum (Garden pea).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Vicieae, Pisum.
                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
US DOE Joint Genome Institute;
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Bryant D., Schmutz J., Larimer F., Land M., Kyrpides N., Ivanova N., Richardson P.;
"Complete sequence of Chlorobium chlorochromatii CaD3.";
Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Shoot,
MEDLINE-2417727; PubNed=12529541; DOI=10.1104/pp.012963;
Davidson S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.;
Davidson S.E., Elliott enches ent-kaurenoic acid oxidase.";
Plant pea gene NA encodes ent-kaurenoic acid oxidase.";
Plant Physiol. 131:335-344(2003).
-!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                  Leucyl-tRNN synthetase class Ia (BC 6.1.1.4).
OrderedLocusNames=Cag_1688;
OrderedLocusNames=Cag_1688;
Orlorobium chlorochomatii (strain CaD3).
Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae; Chlorobium/Pelodictyon group; Chlorobium.
                                                                                                                                                                                                                                                                                                                                                                                                                 55.1%; Score 54; DB 2; Length 805; 61.5%; Pred. No. 11; 2; Indels iive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                      EMBL; CP000108; ABB28940.1; -; Genomic_DNA.
GO; GO:000523; F:RYP binding; IEA.
GO; GO:0004823; F:Leucine-tRNA ligase activity; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0006429; F:leucyl-tRNA aminoacylation; IEA.
Aminoacyl-tRNA synthetase; Complete proteome; Ligase.
SEQUENCE 805 AA; 92007 NW; A0C78BB3732AF54C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
-!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF537321, AAC23063.1; -; mRNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0020037; F:heme binding; IEA.
GO; GO:005506; F:iron ion binding; IEA.
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:004497; F:monooxygenase activity; IEA.
           22-NOV-2005, integrated into UniProtKB/TrEMBL 22-NOV-2005, sequence version 1. 21-FEB-2006, entry version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2003, integrated into UniProtKB/TrEMBL, 01-JUN-2003, sequence version 1. 07-FEB-2006, entry version 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003, sequence version 1.
07-FEB-2006, entry version 21.
Ent-kaurenoic acid oxidase.
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Ouery Match

Bost Local Similarity 61.50,

Bost Local Similarity 61.50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           622 GISRFLGKVWRFV 634
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                                                                                                                         NCBI_TaxID=340177;
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Q84ZW1 PEA
ID Q84ZW1 PEA
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                InterPro; IPR001138; Cytochrome_P450.
InterPro; IPR002401; EP4501.
PANTHER; PTRR19383; Cytochrome_P450; 1.
PANTHER; PTRR19383; Cytochrome_P450; 1.
PRINTS; PR00463; EP450; 2.
PRINTS; PR00463; EP450.
PRINTS; PR001865; CYTOCHROME P450; UNKNOWN 1.
Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding; Monocoxygenaes; Oxtdoreductase.
SEQUENCE 488 AA; 56478 MW; 503453CB6E43C830 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium leguminosarum bv. viciae.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                   Length 488
                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                   Score 53; DB 2;
Pred. No. 9.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF273216; AAG25076.1; -; Genomic_bnA.
                                                                                                                                                                                                                                                                                                               2; Mismatches
GO; GO:0006118; P:electron transport; IBA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QPF7V7_RHILV PRELIMINARY; PRT; Q9F7V7;
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                                                                                                                                                                                                                                                                   54.1%;
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les 9; Conservative
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MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
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Q49LS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Membrane;
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SEQUENCE
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TRANSMEM
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XKR7 PANTR
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  OSCIPLIA
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01-MAR-2005, sequence version 1.
07-FBB-2006, entry version 8.
XK-related protein 7.
Name=XKR7; Synonyms=C20orf159, XRG7;
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Euarchontoglires; Primates; Catarrhini; Hominidae,
                                                        Gaps
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                                                                                                                                                                                                                                                                                                                               "Massive genome erosion and functional adaptations provide insights into the symbiotic lifestyle of Sodalis glossinidius in the tsetse hast ";
                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                   STRAIN-Morsitans,
Toh H., Weiss B.L., Perkin S.A.H., Yamashita A., Oshima K.,
Hattori M., Aksoy S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 51.0%; Score 50; DB 2; Length 361; Best Local Similarity 69.2%; Pred. No. 21; Matches 9; Conservative 1; Mismatches 3; Indels
                                Length 735;
                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
  PROSITE; PS50990; PEPTIDASE C39; 1.
SEQUENCE 735 AA; 80717 MW; 0216259241F3630C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               361 AA; 40247 MW; 1257F70F3C3CA6EC CRC64;
                                 52.0%; Score 51; DB 2; 56.2%; Pred. No. 30;
                                                                                                                                                                            07-FEB-2006, integrated into UniProtKB/TrEMBL. 07-FEB-2006, sequence version 1. 07-MAR-2006, entry version 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                         361 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP008232; BAE74260.1; -; Genomic_DNA.
                                                       3; Mismatches
                                                                                                                                                                                                              Putative glycosyltransferase.
ORFNames=SG0985;
Sodalis glossinidius str. 'morsitans'
                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vertebrates and invertebrates."
                                                                                                   161 GFRWFLPAIWRYRRAF 176
                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 16:149-156(2006)
                                                                              1 GIRRFIGSIWRFLRAF 16
                                                                                                                                                                                                                                                       Enterobacteriaceae; Sodalis.
NCBI_TaxID=343509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 RFIGSIWRFLRAF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :|| |||| ||
RDVGSFWRFLSAF 74
                                  Query Match
Best Local Similarity 56.2<sup>3</sup>
Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                  RESULT 5
Q2NUBS_SODGL
ID Q2NUBS_SODGL
AC Q2NUBS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XKR7 HUMAN
Q5GH72; Q9NUG5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
XKR7_HUMAN
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Matches
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RA Deloukas P., Natthews L.H., Ashurst U.L., Burton J., Gilbert J.G.R., RA Deloukas P., Marthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R., Boloukas P., Marthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R., Balley J., Bartow K.F., Bates K.N., Beard L.M., Beare D.M., Ra Beasley O.P., Bird C.P., Blutler A.P., Carder C., Carter N.P., Clapper D.C., Clamp M., Clark S.Y., Clee C.M., RA Clapper S., Colbley V.E., Collier R.E., Connor R.E., Corby N.R., R., Collson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., Collson A., Coville G.J., Fraser A., French L., Garner P., RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., RA Minckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., RA Lehvæslainho M.H., Leversha M.A., Lioyd C., Lloyd D.M., Lovell J.D., RA Minn S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Parker A., Parker R.A., Parker A., Patch R., Paul R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Racey A., Tromans A.C., Vaudin M., Wall M., Walliams L., Williams S.A., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Waders J., Water B., Willey D.L., Williams L., Williams S.A., Racers J., Waders J., Durbin R.M., Bentley D.R., Beck S., Ra Rocers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The DNA sequence and comparative analysis of human chromosome 20.";
Nature 414:865-871(2001).
-!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential).
-!- SIMILARITY: Belongs to the XK family.
-!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 34;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential.
D8D0FF64B9EDD53D CRC64;
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/FIId=PRO_0000190788.
Potential.
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EMBL; AL031658; CAB88102.1; ALT_SEQ; Genomic_DNA.
Ensembl; ENSG0000101321; Homo Gapiens.
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07-FEB-2006, entry version 6.
XK.related protein 7.
Name=XKR7; Synonyms=XRG7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63826 MW;
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190 LGQVWRYLRALY 201
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Matches 7; Conservative
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355
384
415
579 AA;
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Potential

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580 AA;
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Best Local Similarity
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89
303
326
335
415
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ID Q7VV93_BORPE
AC Q7VV93;
                                                                                                                                                                                                                                                                                                                                                      XKR7 RAT
Q5GH56;
TRANSMEM
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XKR7_RAT
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                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1] —

NUCLECTIDE SEQUENCE [MRNA].

STRAIN=C57BL/6J;

Huang C.-H., Chen Y.;

"A superfamily of XK-related genes (XRG) widely expressed in vertebrates and invertebrates.";

Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

-1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
                                                                                                                                Vertebrates and invertebrates...
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-- SUBCELLUTAR LOCATION: Membrane; multi-pass membrane protein
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0
                                                                                       Huang C.-H., Chen Y.; "A superfamily of XK-related genes (XRG) widely expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 579;
34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6DFE1191093E85D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2005, integrated into UniProtKB/Swiss-Prot. 01-MAR-2005, sequence version 1. 07-FBB-2006, entry version 10. Nak-related protein 7. Name=kKr7; Synonyms=krg7; Muse musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XX-related protein 7.
/FTId=PRO_0000190789.
Potential.
                                                                                                                                                                                                                                                                                                                XX-related protein 7./FIId=PRO_0000190790.Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50; DB 1
Pred. No. 34;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AY534253; AAT07102.1; -; mRNA.
Ensembl; ENSMU560000042631; Mus musculus.
AGI; MGI:3526711; Xkr7.
Membrane; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential).
-!- SIMILARITY: Belongs to the XK family.
                                                                                                                                                                            (Potential).
                                                                                                                                                                                                                                                                                                                                                                                       Potential.
Potential.
Potential.
Potential.
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                                                                                                                          vertebrates and invertebrates.
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                                                                       NUCLEOTIDE SEQUENCE [MRNA].
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Best Local Similarity 58.3
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190 LGQVWRYLRALY 201
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                                                                                                                                                                                                                                                                                                     Membrane, Transmembrane
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109
280
334
404
435
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384
415
579 AA;
                    Pan.
NCBI_TaxID=9598;
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XKR7_MOUSE
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentía; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley;
Huang C.-H., Chen Y.;
"A superfamily of XK-related genes (XRG) widely expressed in
vertebrates and invertebrates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-: SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
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Pred. No. 34;
3; Mismatches 2; Indels
                                                                                                                                             51.0%; Score 50; DB 1; Length 580; 58.3%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential.
8F4907F391B4F5BE CRC64;
                                                                                                              F3291FABF4C5A826 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XK-related protein 7. /FTId=PRO_0000190791. Potential.
                                                                                                                                                                                                                                                                                                                                                               11-OCT-2005, integrated into UniProtKB/Swiss-Prot
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                                                                                                                                                                                                                                                                                                                                  580 AA.
                                                                                                                                                                Pred. No. 34;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential).
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Potential.
Potential.
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Potential
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Potential
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Membrane; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muroidea; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2005, sequence version 1.
07-FEB-2006, entry version 8.
XK-related protein 7.
Name=Xkr7; Synonyms=Xrg7;
                                                                                                               64302 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64338 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [MRNA].
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190 LGQVWRYLRALY 201
                                                                                                                                                              Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                     :| :||:||| |
190 LGQVWRYLRALY 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                                                6 IGSIWRFLRAFY 17
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260
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580 AA;
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Q7WL31_BORBR
Q7WL31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7WL31
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                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=12822 / ATCC BAA-587;
MEDLINE=2287954; PubMed=12910271; DOI=10.1038/ng1227;
MEDLINE=2287954; PubMed=12910271; DOI=10.1038/ng1227;
MEDLINE=2287954; PubMed=12910271; DOI=10.1038/ng1227;
MACHILL J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
Achtman M., Atkin R., Collins M., Cronin A., Davis P., Doggett J.,
Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
                                                                                                                                                                                    Parkhill J., Sebaina M., Preston A., Murphy L.D., Thomson N.R., Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L., Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A., Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., Chillingworth T., Collins M., Cronin A., Davis P., Doggett J., Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C., Sharp S., Slamonds M., Skelton J., Squares R., Squares S., Stevens K., Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
                                                                                                                                                                                                                                                                                                                                    "Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapertussis and Bordetella bronchiseptica.";
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                  Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIOCYS; BPERSE20: PRATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004672; F:ATP binding; IEA.
GO; GO:000468; P:protein Amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot_kinase.
Probom; PR000001; Prot_kinase; 1.
Complete proteome; Hypotherical protein; Kinase; Transferase.
SEQUENCE 278 AA; 31507 MW; 66DDEBFID728D768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB 2; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=TOhama I / ATCC BAA-589 / NCTC 13251;
MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003, integrated into UniProtKB/TrEMBL
integrated into UniProtKB/TrEMBL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BX640419; CAE43065.1; -; Genomic_DNA.
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTW7P3 BORPA PRELIMINARY; PRT; Q7W7P3;
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21-FEB-2006, entry version 14.
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GVRRGISYVLRYLRAFF 63
                              21-FEB-2006, entry version 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%;
                                                                                                                                                                                                                                                                                                                                                                     Nat. Genet. 35:32-40(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.9%;
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                                                          OrderedLocusNames=BP2792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 50.0
Best Local Similarity 52.9
Matches 9; Conservative
                                                                         Bordetella pertussis.
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                                            Aypothetical protein
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                                                                                                                 NCBI_TaxID=520;
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CSTRAIN-EBBSO / ATCC BAA-588;

MEDLINE-22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE-22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE-22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE-22827954; PubMed=12910271; DOI=10.1038/ng1227;

MARTIS D.E., Holden M.T.G., Churcher C.M., Martis B., Quail K.L.,

Anthan M., Atkin R., Baker S., Basham D., Baston N., Cherevach I.,

Anthan M., Atkin R., Baker S., Basham D., Baston N., Cherevach I.,

Anthan M., Atkin R., Hamlin M., Cronin A., Davis P., Doggett J.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin D., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

"The Comparative analysis of the genome sequences of Bordetella pertussis,

"The Comparative analysis of the denome sequences of Bordetella pertussis,

"The Comparative analysis of the genome sequences of Bordetella pertussis,

"The Comparative analysis of the genome sequences of Bordetella pertussis,

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Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K., Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Unwin L., Whitehead S., Barrell B.G., Maskell D.J.; "Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, BX640430; CAE31766.1; -; Genomic_DNA.

BioCyc; BPAR519:BPP2471-MONOMER; -.

GO, GO:0003524; F:ATP binding; IEA.

GO; GO:0004672; F:protein kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR00719; Prot_kinase.

Probom; PHO00001; Prot_kinase; 1.

Complete proteome; Hypothetical protein; Kinase; Transferase.

SEQUENCE 278 AA; 31565 MW; 11DDFD84EFEEFBDF CRC64;
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BioCyc; BBR0518:BB1918-MONOMER; -
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004672; F:protein kinase activity; IEA.
GO; GO:0006408; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot_kinase.
ProDom; PD000001; Prot_kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49; DB 2;
Pred. No. 23;
4; Mismatches
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21-FEB-2006, entry version 14.
Hypothetical protein.
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47 GVRRGISYVLRYLRAFF 63
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NCBI_TaxID=518;
                                                                                                                                                                                                                                                                               Nat. Genet. 35:32-40(2003)
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nes 9; Conservative
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Gaps

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                                      US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annocation of the draft genome assembly of Burkholderia cenocepacia AN 1054.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                        -i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 50.0%; Score 49; DB 2; Length 408; Best Local Similarity 41.2%; Pred. No. 35; Matches 7; Conservative 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 408 AA; 45545 MW; 3C2BCA9471BAAE93 CRC64;
                                                                                                                                                                                                                                                                                                   EMBL; AAHI01000010; EAM12352.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 GIROMLGHVWQWTRSSY 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 41.2 es 7; Conservative
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STRAIN=H12424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=331272;
                        STRAIN=AU 1054;
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Q4LK44;
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9BURK
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Matches
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Q4LK44_
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                                                                                                                                                                                                                                                                                                                                                                                                                  OrderedLocusNames=Bcep18194 A3207;
Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760
/ NCIB 9086 / R18194)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US DOE Joint Genome Institute;
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M., Vergez L., Schmutz J., Larimer F., Land M., Kyrpides N., Lykidis A., Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=AU 1054;
US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
AU 1054.";
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                                                                      Gaps
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Burkholderia cenocepacia AU 1054.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete sequence of chromosome 1 of Burkholderia sp. 383.";
Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
                   50.0%; Score 49; DB 2; Length 278; 52.9%; Pred. No. 23; ive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Length 407;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; CP000151; ABB06809.1; -; Genomic_DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                           22-NOV-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                               407 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      408 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 49; DB
Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q456F4 9BURK PRELIMINARY; PRT;
Q456F4;
                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                   22-NOV-2005, sequence version 1. 21-FEB-2006, entry version 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-SEP-2005, sequence version 1. 07-FEB-2006, entry version 2. Hypothetical protein.
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                                                                                                                  1 GIRRFIGSIWRFLRAFY 17
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                                                                                                                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity 41.2%;
Matches 7; Conservative
                                                                                                                                               47 GVRRGISYVLRYLRAFF
Query Match
Best Local Similarity 52.3.
Best Jocal 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=331271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=269483;
                                                                                                                                                                                                                                                O39157 BURS3
ID G39157 BURS3
ID G39157 BURS3
ID Z2-NOV-2005, int
DT Z2-NOV-2005, sec
DT Z2-NOV-2005, sec
DE Hypothetical proces
ON CHORTEGIAL SPOONS
ON COOPLINE SEQUING
RA COPELAND A, LAURA
RA COMPLETE SEQUING
CC COPYTIQUE SEQUING
CC COPTINE COP
CC COPPLICATION COP
CC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                            Burkholderia cenocepacīa H12424.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 49; DB 2; Length 408; 41.2%; Pred. No. 35; 4; Indels vative 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H12424."; Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AAHLO1000063; EAM16412.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 408 AA; 45603 MW; 7F393888305911D2 CRC64;
                                                               02-AUG-2005, integrated into UniProtKB/TrEMBL.
408 AA.
PRELIMINARY; PRT;
                                                                                                         02-AUG-2005, sequence version 1. 07-FEB-2006, entry version 2. Hypothetical protein.
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Search completed: May 19, 2006, 14:38:13 Job time : 116.429 secs

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22, Appli
61, Appli
11, Appli
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61, Appli
78, Appli
137, Appli
137, Appli
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140, Appli
141, Appli
142, Appli
142, Appli
144, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 242, Application US/08940095
Sequence 242, Application US/08940095
Patent No. 600425
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Grante, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
                                                                                                          Sequence
Sequence
Sequence
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PCT-US93-07545-2
US-08-480-190-1
US-08-480-190-61
US-08-488-379-61
US-08-488-379-61
US-08-475-399A-61
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US-08-127-954-138
US-08-127-954-141
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REGISTRATION NUMBER: 30,742
REPERONCE/DOCKET NUMBER: 009196-0004-999
TELEPHONE: 650-493-4935
TELERAX: 650-493-556
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
TIPORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-08-127-954-144
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ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESQ Version 2.0
CURRENT APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-5EP-1997
CLASSIFICATION NUMBER: STENCY APPLICATION NUMBER: FILING DATE: SPEDICATION NUMBER: FILING DATE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Ameri
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US-08-940-095-242
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
           US-08-940-095-242
             Sequence 242, App Sequence 342, App Sequence 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
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/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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63.384 Million cell updates/sec
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Sequence 3, 1
Sequence 3, 1
Sequence 2, 1
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Sequence 2, 1
Sequence 2, 1
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                                                                                                                                                                                                ; Search time 24.8571 Seconds
                                    GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-940-095-242
US-08-940-093-242
US-09-465-719-242
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US-09-453-818-242
US-09-453-813-242
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US-09-205-258-892
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US-08-07-2558-892
US-08-08-75-399A-3
US-08-077-255A-3
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US-08-488-379-2
US-08-475-399A-2
US-08-077-255A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650591 seqs, 87530628 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                            1 GIRRFIGSIWRFLRAFYG 18
                                                                                                                                                                                                   May 19, 2006, 14:38:42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                     US-10-712-447-117
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Match Length
                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                      Run on:
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STRANDEDNESS:
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US-09-465-719-242
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                                                                                                                                                                                                            Sequence 242, Application US/08940093

Fatent No. 6037323

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Buttner, Klaus

APPLICANT: Growth, Isabelle

APPLICANT: Growth, Isabelle

APPLICANT: Metz, Gunther

ITILE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

ITILE OF INVENTION: APOLIPOPROSES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Score 74; DB 2; Length 18;
Pred. No. 4.8e-05;
6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTY: USA

ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 29-5EP-1997
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 39-742
REFERENCE/DOCKET NUMBER: 30-742
REFERENCE/DOCKET NUMBER: 30-742
REFERENCE/DOCKET NUMBER: 30-742
REFERENCE/DOCKET NUMBER: 650-493-4935
TELEFAX: 650-493-4935
TELEFAX: 650-493-4935
TELEFAX: 651-493-4935
TELEFAX: 651-493-4935
SEQUENCE CHARACTERISTICS:
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US-08-940-096-242
Sequence 242, Application US/08940096
; Patent No. 6046166
, GENERAL INFORMATION:
                                                                                                          1 GIRRFIGSIWRFLRAFYG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GIRRFIGSIWRFLRAFYG 18
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US-08-940-093-242
  Query Match
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 61.19
Matches 11; Conservative
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Gaps
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Rabels
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                      COMPOTER: IBM COMPATIBLE
COMPOTER: IBM COMPATIBLE
COMPOTER: IBM COMPATIBLE
CONTREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
CLASSIFICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
ATORNEY/AGENT INFORMATION:
NAME: COTTAIL AUGUST
REFERENCE/DOCKET NUMBER: 30,742
RECISTRATION NUMBER: 30,742
RECISTRATION NUMBER: 30,742
RECISTRATION NUMBER: 30,742
RECISTRATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 242, Application US/09465719
Patent No. 6265377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELERAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GIRRFIGSIWRFLRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: No. 6046166e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 75.5
Best Local Similarity 61.1
Matches 11; Conservative
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COUNTRY:
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COMPUTER: IEM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FeatSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,838
FILING DATE:
CLASSIFICATION:
PRICA APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                  REFERENCE/DOCKET NUMBER: 005
TELECHONE: 650-493-4935
TELEPHONE: 650-493-5556
TELEFAX: 650-493-5556
TELERAX: 65141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-453-838-242
; Sequence 242. Application US/09453838
Patent No. 6376464
; Patent INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GIRRFIGSIWRFLRAFYG 18
                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: No. 6376464e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 75.5%;
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO
SEQUENCE CHARACTER.FSTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 4.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Land Compatible
OCHUTER: Land Compatible
OCHUTER: Land Compatible
OCHUTER: Land Compatible
COMPUTER: Land Compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
FILING DATE:
CLASSIFICATION NUMBER: 08/940,093
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA RESERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEFAX: 650-493-4935
TELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IEM Compatible
COMPUTER: IEM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,605
FILING DATE: 26-NO. 632341-1999
CLASSIFICATION: VUNKNOWN:
PRIOR APPLICATION NUMBER: 08/940,095
FILING DATE: CUNKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 242, Application US/09453605
Patent No. 6129341
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GIRRFIGSIWRFLRAFYG 18
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1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6265377e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.5%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 61.11
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-465-719-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-453-605-242
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Gornut, Isabelle
APPLICANT: Ocrunt, Isabelle
APPLICANT: Dufourcq, Jean
APPLICANT: Dufourcq, Jean
APPLICANT: MOLOIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ANDRESCOUR
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                      Length 18;
                                                                                                                                                                                                                                                                                                                                                 Score 74; DB 2; Length 18;
Pred. No. 4.8e-05;
6; Mismatches 1; Indels
009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/ABENT INFORMATION:
NAME: COTUZZI, Lauta A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: NO. 632931e
SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-453-605-242
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Sequence 242, Application US/09453841
Patent No. 6573239
GENERAL INFORMATION:
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US-09-453-833-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NY COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
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Sequence 242, Application US/08940136

Patent No. 6518412

GENERAL INFORMATION:

APPLICANT: Basseux, Jean-Louis

APPLICANT: Buttner, Klaus

APPLICANT: Cornut, Isabelle

APPLICANT: Cornut, Isabelle

APPLICANT: Cornut, Osan

TITLE OF INVENTION: GENE THERAPY APPROACHES TO

TITLE OF INVENTION: GENE THERAPY APPROACHES TO

TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

NUMBER OF SEQUENCES: 274

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                Query Match
75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 75.5%; Score 74; DB 2; Length 18; 1 Similarity 61.1%; Pred. No. 4.8e-05; 11; Conservative 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCEZ DOCKET NUMBER: 009196-0007-999
TELECOMMUNICATION INPORMATION:
TELEPHONE: 650-493-4935
TELEPAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IRM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTEGO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,136
FILING DATE: 29-SEP-1997
CLASSIFFCATION: 514
PR.OR. APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
FILING DAT
                                                                                                                                                                                                                                                                                                     1 GIRRFIGSIWRFLRAFYG 18
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6518412e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-08-940-136-242
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                 US-09-453-838-242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Sequence 242, Application US/09453833

Patent No. 6602854

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Sekul, Renate

APPLICANT: Sekul, Renate

APPLICANT: Gunther, Klaus

APPLICANT: Gunther

APPLICANT: Dufourcq, Jean

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Duffourcy, Jean
APPLICANT: Duffourcy, Jean
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
TOWNERS OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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ER: 009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastESQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUER A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pennie & Edmonds LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: COTUZZÍ, LAUTA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GIRRFIGSIWRFLRAFYG 18
                                                                                                                                                                                                                                                                                                                                                           COUMIAN: .....
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: No. 6573239e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM COM
OPERATING SYSTEM:
SOFTWARE: FASTSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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RESULT 8 US-09-453-841-242

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APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                             75.5%; Score 74; DB 2; 1
61.1%; Pred. No. 4.8e-05;
    APPLICATION NUMBER: 08/940,095
FILING DATE: ATTORNEY/AGENT INFORMATION:
NAME: COUNZI, LBULTA A
RECISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECHONE: 650-493-4935
TELEFAX: 650-493-556
TELEFAX: 650-493-556
TELEFAX: 650-493-6955
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,840
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 242, Application US/09453840 Patent No. 6716816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GIKKFLGSIWKFIKAFVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GIRRFIGSIWRFLRAFYG 18
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: No. 6630450e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                           LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 61.1<sup>1</sup>
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                       US-09-453-826-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-453-840-242
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APPLICANT: Schul, Renate
APPLICANT: Cornut, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 75.5%; Score 74; DB 2; 1 Best Local Similarity 61.1%; Pred. No. 4.8e-05; Matches 11; Conservative 6; Mismatches 1;
                                                                                                                                                                                                                                                                                                                             APPLICALION
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME:
CCUZZI, LAUKA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPAK: 650-493-4935
TELEPAK: 650-493-5556
TELEX: 66141 PENNIE
JINFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036-2811
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: ISM Compatible
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FRASESQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,833
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 242, Application US/09453826
Patent No. 6630450
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
FOOLOGY: linear
MOLECULE TYPE: No. 6602854e
US-09-453-833-242
                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                        New York
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CLASSIFICATION:
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                                                                 USA
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Coruzzi, Laura A REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 005 TELECOMMUNICATION INFORMATION: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GIRRFIGSIWRFLRAFYG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: No. 6753313e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
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                                                                                                                                                                                                                                                                                                                                            New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-283-599-242
                                     US-09-453-834-242
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                                                                                                                                                                                                                                                                                                                                                                                                              Butther, Klaus
Cortnut, Isabelle
Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                              Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:

NAME: COTUZZI, LAUTA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEFXX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
                                                                                                              75.5%; Score 74; DB 2; I
61.1%; Pred. No. 4.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OCMPUTER: IBM Compatible
OCMPUTER: TRANSTER: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATE:
FILING DATE: 25-May-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear in MOLECULE TYPE: No. 6734169e ; SEQUENCE DESCRIPTION: SEQ ID NO: 242: US-09-865-989-242
                                                                                                                                                                                                                                                                                                                        Sequence 242, Application US/09865989
Patent No. 6734169
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 18 amino acids
                                                                                                                                                                                                               ||::|:||||:|:|| |
| GIKKFLGSIWKFIKAFVG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 258
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6716816e
                                                                                                                                                                                                                                                                                                                                                                                                        Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                Best Local Similarity 61.1 Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
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Best Local Similarity
Matches 11; Conserv
                                                                           US-09-453-840-242
                                                                                                                                                                                                                                                                                                         US-09-865-989-242
                                                                                                                  Query Match
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Gaps
Sequence 242, Application US/09453834
Sequence 242, Application US/09453834
GENERAL INFORMATION:
APPLICANT: Dassente:
APPLICANT: Sekul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Gornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 25CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buttner, Klaus
Cornut, Isabelle
Merz, Gunther
Dufourcg, Jean
VENTION: GENE THERAPY APPROACHES TO
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Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10005-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,834
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 242. Application US/10283599
; Patent No. 6844327
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
TITLE OF INVENTION: SUPPLY APPLITITE OF INVENTION: SUPPLY APPLICANT:
TITLE OF INVENTION: SUPPLY APPLICANT: Metz, Gunther
TITLE OF INVENTION: ```

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LENGTH: 18 amino acids
  TYPE: amino acid
STRANDEDNESS: single
   TOPOLOGY: linear
  US-09-465-718-242
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   Sequence 242, Application US/09465718

| Sequence 242, Application US/09465718
| Patent No. 6900177
| GENERAL INFORMATION:
| APPLICANT: Dasseux, Jean-Louis |
| APPLICANT: Batcher, Klaus |
| APPLICANT: Genut, Isabelle |
| APPLICANT: Merz, Gunther |
| APPLICANT: Merz, Gunther |
| APPLICANT: Merz, Gunther |
| TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS |
| TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS |
| TORRESPONDENCES: 258 |
| ADDRESSEE: Pennie & Edmonds LLP |
| STREET: 1155 Avenue of the Americas |
| CITY, New York |
| CITY New York |
| CI
  Gaps
  ö
TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

NUMBER OF SEQUENCES: 274

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
   Length 18;
  1; Indels
   Score 74; DB 2; I
Pred. No. 4.8e-05;
  009196-0007-999
  6; Mismatches
  ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYBE: Diskette
COMPUTER: PAPELICATION
CURRENT APPLICATION NUMBER: US/10/283,599
FILING DATE: 29-OCT-2002
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/283,599
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 009196-000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 660-493-5556
TELEFAX: 66141 PENNIE
TELERAX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
   1 GIRRFIGSIWRFLRAFYG 18
   1 GIKKFLGSIWKFIKAFVG 18
  ) TOPOLOGY: linear
; MOLECULE TYPE: No. 6844327e
US-10-283-599-242
   Query Match
Best Local Similarity 61.1%;
Matches 11; Conservative
  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
   TYPE: amino acid
STRANDEDNESS: single
  USA
   US-09-465-718-242
  COUNTRY:
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Appl Appl Appl Appl Appl Appl Appl

Sequence:

Run on:

Searched:

Database

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Sequence 2, Application US/10712447

Sequence 2, Application No. US20040186057A1

CENERAL INFORMATION:

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GESTA

TITLE OF INVENTION: SYRTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: SYRTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIFOPROFIEIN E AND METHODS OF USE

FILE REFERENCE: 112739-123US

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2002-11-13

PRIOR FILING DATE: 2002-11-13
  Gaps
  APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: GARBER, DAVID W.
APPLICANT: GARBER, DAVID W.
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE FILE REPERSENCE: 112739-123US
CURRENT APPLICATION NUMBER: US 003-11-13
PRIOR APPLICATION NUMBER: 60/425,821
PRIOR APPLICATION NUMBER: 60/425,821
PRIOR PLILING DATE: 2003-11-13
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PATENTIN VET: 3.2
  Sequence 4
Sequence 1
Sequence 2
Sequence 3
Sequence 3
  Sequence
Sequence
Sequence
                       Sequence
   Sequence
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Sequence
  Sequence
Sequence
  OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
  Sequence
  ö
   Length 18;
  Indels
   100.0%; Score 98; DB 4; I
llarity 100.0%; Pred. No. 9.2e-08;
Conservative 0; Mismatches 0;
US-10-712-447-22
US-10-712-447-78
US-10-712-447-120
US-10-712-447-130
US-10-712-447-56
US-10-712-447-56
US-10-712-447-79
US-10-712-447-79
US-10-712-447-94
US-10-712-447-97
US-10-712-447-97
US-10-712-447-97
US-10-712-447-97
   ALIGNMENTS
  ; Sequence 117, Application US/10712447; Publication No. US20040186057A1; GENERAL INFORMATION:
  1 GIRRFIGSIWRFLRAFYG 18
   TYPE: PRT
ORGANISM: Artificial Sequence
   Similarity
18; Conserv
   2 1 1 1 1 1 1 1 1 1 1
  , 'RESULT 1
US-10-712-447-117
   US-10-712-447-117
   RESULT 2
US-10-712-447-2
   SEQ ID NO 117
LENGTH: 18
       80
80
80
80
77
78
77
77
77
76
   Query Match
Best Local S
   F 19 645 4
   FEATURE
  Best Loca
Matches
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   a
  91, Appl
21, Appl
34, Appl
4, Appl
113, App
99, Appl
112, App
114, Appl
17, Appl
  Sequence 10, Appl
Sequence 13, Appl
Sequence 115, App
Sequence 116, App
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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i Sequence 5, Application US/10712447
i Publication No. US20040186057A1
i GENERAL INFORMATION:
i APPLICANT: ANATHRARMIAH, GATTADAHALLI M.
i APPLICANT: DATTA, GEETA
i TILLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES MIMICKING
i TILLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
i TILLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
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i TILLE OF INVENTION UNUBER: US/10/712,447
i CURRENT FILING DATE: 2003-11-13
i PRIOR PILING DATE: 2002-11-13
i NUMBER OF SEQ ID NOS: 210
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i LENGTH: 18
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Sequence 8, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:

APPLICANT: GARBER, DAVID W.

APPLICANT: GARBER, DAVID W.

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION APOLIPOPROTEIN E AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT FILING DATE: 2003-11-13

PRIOR FILING DATE: 2003-11-13

NUMBER OF SEQ ID NOS: 210
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US-10-712-447-13

Sequence 13, Application US/10712447

Publication No. US20040186057A1

GENERAL INFORMATION:
APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
APPLICANT: GARBER, DAVID W.
APPLICANT: GARBER, DAVID W.
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILE REFERENCE: 112739-123US
CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT APPLICATION NUMBER: 60/425,821

PRIOR PILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: Patentin Ver. 3.2

LENGTH: 18
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US-10-712-447-10

i Sequence 10, Application US/10712447

j Sequence 10, US20040186057A1

j GENERAL INFORMATION:
    APPLICANT: ANNTHARAMIAH, GATTADAHALLI M.

APPLICANT: APPLICANT DATTA, GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT PILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENTIN Ver. 3.2

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88.9%; Pred. No. 3.7e-07;
tive 2; Mismatches 0;
  .7e-07;
  95.9%; Score 94; DB 4;
88.9%; Pred. No. 3.7e-07
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ORGANISM: Artificial Sequence
PEATURE:
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Matches 16; Conservative
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Matches 16, Conservative
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US-10-712-447-127
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Sequence 116, Application US/10712447

Sequence 116, Application US/10712447

Publication No. US20040186057A1

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: APPLICANT: GEETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYBEPTIDES MIMICKING

TITLE OF INVENTION: APPLICANTION: APPLIC
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   Sequence 115, Application US/10712447

Sequence 115, Application US/10712447

Sequence 115, Application US/10712447

GENERAL INFORMATION:
APPLICANT: AGARREK.
APPLICANT: AGARREK.
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
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TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES
TITLE OF INVENTION: 2021.1239-12308

CURRENT APPLICATION NUMBER: 06/425,821

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

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SEQ ID NO 115

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Sequence 129, Application US/10712447

Publication No. U520040186057A1

GENERAL INFORMATION:

APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

APPLICANT: DATTA, GETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APOLIPPOPROTEIN E AND METHODS OF USE

FILE REFERENCE: 112739-123US

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT APPLICATION NUMBER: 05/425,821

PRIOR APPLICATION NUMBER: 2003-11-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: Patentin Ver. 3.2

LENGTH: 18
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APPLICANT: GARBER, DAVID W.
APPLICANT: GARBER, DAVID W.
APPLICANT: DATTA, GEETA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
FILE REFERENCE: 112739-123US
CURRENT APPLICATION NUMBER: US/10/712,447
CURRENT FILING DATE: 2003-11-13
PRIOR FILING DATE: 2002-11-13
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US-10-712-447-129
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US-10-712-447-127
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2; Mismatches 0; Indels
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Pred. No. 3.7e-07;
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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Subblication No. US20040186057A1
GENERAL INFORMATION:
APPLICANT: ANTHARAMIHA, GATTADAHALLI M.
APPLICANT: GARBER, DAVID W.
APPLICANT: GARBER, DAVID W.
TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN FOLLYPEPTIDES MIMICKING
TITLE OF INVENTION: SYNTHETIC SINGLE DOWAIN POLYPEPTIDES
GURRENT APPLICATION NUMBER: US/10/712,447
GURRENT PILING DATE: 2003-11-13
PRIOR FILING DATE: 2003-11-13
PRIOR FILING DATE: 2002-11-13
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; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-12348
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; CURRENT PILING DATE: 2003-11-13
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; PRIOR FILING DATE: 2002-11-13
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LOCATION: (14)
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  Sequence 131, Application US/10712447

Publication No. US20040186057A1

FURNERL INFORMATION:

APPLICANT: ANANTHARIAN, GATTADAHALLI M.

APPLICANT: GARBER, DAVID W.

APPLICANT: GARBER, DAVID W.

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/10/712,447

CURRENT APPLICATION NUMBER: 60/425,821

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 210

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Publication No. US20040186057A1
GENERAL INFORMATION:
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APPLICANT: GARBER, DAVID W.
APPLICANT: DATTA, GEETA
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
TITLE OF INVENTION: APPLICANTON: APPLICANTON: APPLICANTON: APPLICANTON: APPLICANTON: APPLICANTON: APPLICANTON WIBBER: US/10/712,447
CURRENT APPLICATION NUMBER: 05/425,821
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
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US-10-712-447-131
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Sequence 74, Application US/10712447

Publication No. US20040186057A1

PRICANT: AMPRICANT

PAPLICANT: DATTA, GETA

TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

TITLE OF INVENTION: APPLICATION NUMBER: US/10/712,447

CURRENT PILING DATE: 2003-11-13

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Sequence 2947, Application US/10511937

Publication No. US2006008883641

GENERAL INFORMATION:

APPLICANT: EXPRESSION DIAGNOSTICS, INC.

APPLICANT: Fry, Kirk

APPLICANT: Fry, Kirk

APPLICANT: Prentice, James

APPLICANT: Prentice, James

APPLICANT: Mocris, MacDonald

APPLICANT: Morris, MacDonald

PRIOR APPLICATION NUMBER: US 10/131, 931

PRIOR PILING DATE: 2003-04-24

PRIOR PILING DATE: 2002-04-24

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Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-949-925-111

US-11-242-505A-48

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US-11-311-55-16

US-11-311-55-16

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Sequence 18, Application US/11242505A

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  APPLICANT: Sturley, Stephen L
APPLICANT: Sturley, Stephen L
APPLICANT: Turkish, Aaron R
APPLICANT: Billheimer, Jeffrey T
APPLICANT: COMLey, Debra
TITLE OF INVENTION: AWAT-RELATED METHODS AND ARTICLES
FILE REPERENCE: 0575/72796/JPW/ALM/JCS
CURRENT APPLICATION NUMBER: US/11/204,427
   Query Match 35.7%; Score 35; DB 7; Best Local Similarity 44.4%; Pred. No. 32; Matches 4; Conservative 4; Mismatches
   Sequence 7, Application US/11204427 Publication No. US20060100146A1 GENERAL INFORMATION:
    35.7%;
  NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.3
    Query Match 35.7
Best Local Similarity 75.0
Matches 6; Conservative
   Query Match 35.7
Best Local Similarity 60.0
Matches 6; Conservative
  8 SIWRFLRAFY 17
  84 AIWRQLRDYY 93
   ORGANISM: Homo Sapiens
  2 IRRFIGSIW 10
  199 WSFLDAFY 206
  ORGANISM: Homo sapiens
  10 WRFLRAFY 17
  US-11-242-505A-18
  US-11-204-427-7
  US-11-204-427-7
   SEQ ID NO 7
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   WESULY 3

WESULY 4

WESULY 4

WESULY 5

SEQUENCE 48, Application US/11242505A

SEQUENCE 48, Application US/11242505A

PUBLICATION NO. US20060099656A1

GENERAL INFORMATION:

APPLICANT: Healy, Aileen

TITLE OF INVENTION: Methods and Compositions for Treating

TITLE OF INVENTION: MABER: US/11/242,505A

CURRENT APPLICATION NUMBER: US 10/290,078

PRIOR FILING DATE: 2002-11-07

PRIOR APPLICATION NUMBER: US 60/347,949

PRIOR FILING DATE: 2002-12-17

PRIOR APPLICATION NUMBER: 60/341,606

PRIOR FILING DATE: 2001-12-17

NUMBER OF SEQ ID NOS: 48

LENGTH: 313

LENGTH: 313

TYPE: PRR

CURRENT SET FRENCE: Mindows Version 4.0

SEQ ID NO 48

LENGTH: 313

TYPE: PRR

CORGANISM: Homo sapiens

US-11-242-505A-48
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   36.7%; Score 36; DB 1; Length 74; 54.5%; Pred. No. 2.8; tive 1; Mismatches 4; Indels
   , OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-111
            FILE REFERENCE: PZO23P2
CURRENT APPLICATION NUMBER: US/09/949,925
CURRENT FLLING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 60/232,150
PRIOR FILING DATE: 2000-12-09
PRIOR FILING DATE: 1999-01-27
PRIOR PILING DATE: 1999-01-27
PRIOR PILING DATE: 1999-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
   Query Match
Best Local Similarity 54.5
Matches 6; Conservative
  2 IRRFIGSIWRF 12
   59 LREVSGKIWRF 69
  ORGANISM: Homo sapiens
  FEATURE:
NAME/KEY: SITE
LOCATION: (74)
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APPLICANT: WADGG, WILLIAM,
APPLICANT: WADGG, WILLIAM,
APPLICANT: WADGG, WILLIAM,
TITLE OF INVENTION: IL-17 HOWOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFREENCE: PISSIRICALIU (US)
CURRENT APPLICATION NUMBER: US/09/747,259
PRIOR APPLICATION NUMBER: US/09/747,259
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR PRIOR PRILING DATE: 1999-12-30
PRIOR PRILING DATE: 1999-12-30
PRIOR PRILING DATE: 2000-01-11
PRIOR PRILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-03-21
  Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 39
  Sequence 6, Application US/11223738
; Sequence 6, Application US/11223738
; Publication No. US20060099682A1
; GENERAL INFORMATION:
    APPLICANT: DELANY, Samantha
; APPLICANT: TATE, Simon Nicholas
; APPLICANT: TATE, Simon Nicholas
; TITLE OF INVENTION: HUMAN VANILLOID RECEPTORS AND THEIR USES
; TITLE OF INVENTION: HUMAN VANILLOID RECEPTORS AND THEIR USES
; CURRENT APPLICATION NUMBER: US/11/223,738
; CURRENT FILING DATE: 2005-09-09
; PRIOR FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-11-30
   35.7%; Score 35; DB 7; Length 667; 43.8%; Pred. No. 58;
   3; Mismatches
  Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
   502 ŘŘLVGALAELÍŘÁALG 517
   3 RRFIGSIWRFLRAFYG 18
   VanLookeren, Menno
Vandlen, Richard
Watanabe, Colin
  Williams, P.Mickey
Wood, William
  Query Match
Best Local Similarity 43.8<sup>3</sup>
Matches 7; Conservative
  Tumas, Daniel
  TYPE: PRT
ORGANISM: Homo Sapien
  US-11-311-561-16
  JS-11-223-738-6
   SEQ ID NO 16
   APPLICANT:
APPLICANT:
APPLICANT:
   APPLICANT:
APPLICANT:
APPLICANT:
  APPLICANT
   g
   APPLICANT: Yangura, Daniel
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
PILE REFERENCE: P1381R1C1P1(US)
CURRENT APPLICATION NUMBER: US/11/311,555
CURRENT FILING DATE: 2005-12-20
  ö
   CURKENT FILLING DATE: 2005-12-20

FRIOR PAPLICATION NUMBER: US/09/747,259

PRIOR PELING DATE: 2000-12-20

PRIOR PELING DATE: 1999-05-14

PRIOR PELING DATE: 1999-05-14

PRIOR PELING DATE: 1999-05-14

PRIOR PELING DATE: 1999-12-30

PRIOR PILING DATE: 1999-12-30

PRIOR PILING DATE: 2000-01-11

PRIOR PILING DATE: 2000-01-11

PRIOR PILING DATE: 2000-01-11

PRIOR PILING DATE: 2000-03-12

PRIOR PILING DATE: 2000-03-14

PRIOR PILING DATE: 2000-03-16

PRIOR PILING DATE: 2000-03-16

PRIOR PILING DATE: 2000-03-21

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  35.7%; Score 35; DB 7; Length 667;
43.8%; Pred. No. 58;
tive 3; Mismatches 6; Indels
  US-11-311-561-16; Sequence 16, Application US/11311561; Publication No. US2006008917A1; GENERAL INFORMATION:
   Grimaldi,Christopher
  || :|:: ||| |
RRLVGALAELLRAALG 517
  3 RRFIGSIWRFLRAFYG 18
   Watanabe, Colin
Williams, P.Mickey
Wood, William
  VanLookeren, Menno
   Vandlen, Richard
   Query Match 35.7
Best Local Similarity 43.8
Matches 7; Conservative
   Li, Hanzhong
Hillan, Kenneth
  Godowski, Paul
:|| :|::|
155 VRRVLGAVW 163
   Tumas, Daniel
   ORGANISM: Homo Sapien
   US-11-311-555-16
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RESULT 12
US-10-504-120-19
; Sequence 19, Application US/10504120
  US-11-302-678-5
   SEQ ID NO 88
   RESULT 11
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  8
  Publication US/11302678
Publication No. US2006008881A1
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Venketeswarlu, Karicheti

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

TITLE OF INVENTION: URCLOGGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,

TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.

TITLE OF INVENTION: 12003, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.

TITLE OF INVENTION: 12002-012PIRM OWNI

CURRENT APPLICATION NUMBER: US/11/302,678

PRIOR PAPLICATION NUMBER: US/10/345,680

PRIOR APPLICATION NUMBER: US 60/349,511
  Sequence 2, Application US/10975692

Publication No. US2006009021A1

Sequence 2, Application US/10975692

Publication No. US2006009021A1

GARDEAL INPORMATION:

APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION

APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION

APPLICANT: WASHINGS JOHN ASSAURES AND METHODS OF USING THEM FOR SYNTHESIS OF

TITLE OF INVENTION: POLYTUSATURATED FATTY ACIDS

CURRENT APPLICATION NUMBER: US/10/975,692

CURRENT FILING DATE: 2001-08-17

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1998-12-07

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 2

LENGTH 447

TUBECH! 447
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  Query Match
34.7%; Score 34; DB 6; Length 447;
Best Local Similarity 43.8%; Pred. No. 53;
Matches 7; Conservative 4; Mismatches 5; Indels
   DB 7; Length 764;
69;
  6; Indels
   h 35.7%; Score 35; DB Similarity 42.9%; Pred. No. 69; 6; Conservative 2; Mismatches
PRIOR APPLICATION NUMBER: GB98263593
PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 6
LENGTH: 764
   ; ORGANISM: Caenorhabditis elegans US-10-975-692-2
  ||: ::|: ||||
130 IRKILETIFTILFAFY 145
   2 IRRFIGSIWRFLRAFY 17
  443 GIYLLVGQLWYFWR 456
   1 GIRRFIGSIWRFLR 14
  TYPE: PRT
ORGANISM: Homo sapiens
   Query Match
Best Local Similarity
Matches 6; Conserv
  US-11-223-738-6
   US-11-302-678-5
   TYPE: PRT
  g
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Sequence 88, Application US/11249111

Sequence 88, Application US/11249111

Sequence 88, Application No. US20060099623A1

Sequence 88, Application No. US20060099623A1

Septicant INPORMATION:

APPLICANT: Glenn, Matthew

APPLICANT: Lubbers, Mark W

APPLICANT: Dekker, James

TITLE OF INVENTION: and methods for their use.

TITLE OF INVENTION: and methods for their use.

TITLE OF INVENTION: and WELOATION WUBBER: US/11/249,111

CURRENT APPLICATION WUBBER: 10/288,930

PRIOR PILING DATE: 2002-11-05

PRIOR PILING DATE: 2000-11-28

PRIOR PILING DATE: 2000-11-28

PRIOR PILING DATE: 1099-12-02

PRIOR PILING DATE: 1099-12-02

NUMBER OF SEQ ID NOS: 124

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   Gaps
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   34.7%; Score 34; DB 7; Length 599; 57.1%; Pred. No. 76; 0; Indels ative 3; Mismatches 0; Indels
  Score 34; DB 7; Length 627; Pred. No. 80;
   2; Indels
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/360,500
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-18
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-08-14
PRIOR PLING DATE: 2002-09-27
PRIOR FILING DATE: 2002-09-27
PRIOR FILING DATE: 2002-09-27
PRIOR FILING DATE: 2002-09-27
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PRIOR FILING DATE: 2002-10-21
PRIOR FILING DATE: 2002-11-05
PRIOR FILING DATE: 2002-11-05
PRIOR FILING DATE: 2002-11-05
PRIOR FILING DATE: 2002-11-05
PRIOR FILING DATE: 2002-11-36
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PASLESEQ for Windows Version 4.0
SENGTH: 599
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  ORGANISM: Lactobacillus rhamnosus US-11-249-111-88
   Query Match
Best Local Similarity 55.6%;
Matches 5; Conservative
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  194 FVGTIWMIL 202
   5 FIGSIWRFL 13
   ORGANISM: Homo Sapiens
   Query Match
Best Local Similarity
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64 LGNVWRF 70
   6 IGSIWRF 12
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   33.7%; Score 33; DB 6; Length 714; 41.7%; Pred. No. 1.4e+02;
  Length 749;
   Score 33; DB 6; Length 651;
Pred. No. 1.2e+02;
3; Mismatches 2; Indels
   generic 443, Application US/10505928

publication No. US20060086532A1

general INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFFWARE: Patentin 3.2
LENGTH: 749
  GENERAL INFORMATION:
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GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 3167-002510US
CURRENT PILLING DATE: 2004-06-14
PRIOR PILLING DATE: 2004-06-14
PRIOR FILLING DATE: 2003-06-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.3
SECTION OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.3
  33.7%; Score 33; DB 6; 1
30.0%; Pred. No. 1.5e+02;
tive 6; Mismatches 1;
   2; Mismatches
  Search completed: May 19, 2006, 15:28:17
  LENGTH: 714

TYPE: PRT

COGANISM: Caenorhabditis elegans
15-10-868-498-2
   Query Match
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Matches 4; Conservative
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Matches 5; Conservative
   Best Local Similarity 30.0
Matches 3; Conservative
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   2 IRRFIGSIWR 11
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; ORGANISM: Homo sapiens
US-10-511-937-2401
  2 IRRFIGSIW 10
   TYPE: PRT
ORGANISM: Homo sapiens
   US-10-505-928-443
  US-10-505-928-443
LENGTH: 651
   Query Match
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       FULLICACION NO. USZOOGGOBBBS2A1
GENERAL INFORMATION:
APPLICANT: EXALINES AND MIRRS AS MODIFIERS OF INSULIN RECEPTOR SIGNALING AND METHODS OF
TITLE OF INVENTION: USE
FILE REFERENCE: EXG3-G03C-PC
CURRENT APPLICATION UNDRER: US/10/504,120
CURRENT APPLICATION UNDRER: 60/358,217
PRIOR APPLICATION NUMBER: 60/358,217
PRIOR PLING DATE: 2002-02-06
PRIOR PRIOR PLING DATE: 2002-02-06
PRIOR PLING DATE: 2002-02-06
PRIOR PRIOR PLING DATE: 2002-02-06
PRIOR PRIOR PRIOR DATE: 2002-02-06
PRIOR PRIOR PLING DATE: 2002-02-06
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PRIOR PLING DATE: 2002-02-06
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PRIOR PLING DATE: 2002-02-06
PRIOR PLING   ö
   Sequence 2401, Application US/10511937

Sequence 2401, Application US/10511937

Publication No. US20060088836A1

GENERAL INPORMATION:

APPLICANT: EXPRESSION DIAGNOSTICS, INC.

APPLICANT: Wooldward, Robert

APPLICANT: Worldsward, Robert

APPLICANT: Prentice, James

APPLICANT: Prentice, James

APPLICANT: Prentice, James

APPLICANT: Prentice, James

APPLICANT: MOSCONAID

APPLICANT: MOSCONAID

APPLICANT: MOSCONAID

APPLICANT: MOSCONAID

APPLICANT: ROSENDETG, Steven

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

TITLE OF INVENTION: MONDIANER: US/10/511,937

CURRENT FILING DATE: 2004-10-19

PRIOR APPLICATION NUMBER: US/10/31,831

PRIOR FILING DATE: 2003-04-24

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  Length 643;
  5; Indels
  33.7%; Score 33; DB 6; I
38.5%; Pred. No. 1.2e+02;
trive 3; Mismatches 5;
  SOFTWARE: Patentin version 3.2
SEQ ID NO 19
LENGTH: 643
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482 QFIDCVWQMTRQF 494
   4 RFIGSIWRFLRAF 16
  Query Match 33.7
Best Local Similarity 38.5
Matches 5; Conservative
  ; ORGANISM: Homo sapiens
US-10-504-120-19
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Job time : 2.14286 secs

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